

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 25, 2003, 15:10:13 ; Search time 14 Seconds

(without alignments)
229.078 Million cell updates/sec

Title: US-09-620-586B-19

Perfect score: 623
Sequence: 1 DFGIDCDHEHTESSRCRCRYPL.....KEGLIYKIPAMVYDNCGS 109

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued_patents_AA:*
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6: /cgn2_6/ptodata/1/1aa/backfilled1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	501	80.4	126	2	US-08-525-596B-6
2	501	80.4	126	3	US-09-177-860A-6
3	501	80.4	126	4	US-09-378-238-6
4	501	80.4	126	4	US-09-451-501-6
5	501	80.4	130	4	US-09-378-238-21
6	501	80.4	225	4	US-09-378-238-19
7	501	80.4	375	2	US-08-525-596B-14
8	501	80.4	375	2	US-08-765-875-5
9	501	80.4	375	3	US-08-795-671-5
10	501	80.4	375	3	US-09-177-860A-14
11	501	80.4	375	4	US-09-252-149B-29
12	501	80.4	375	4	US-09-252-149B-32
13	501	80.4	375	4	US-09-252-149B-34
14	501	80.4	375	4	US-09-252-149B-35
15	501	80.4	375	4	US-09-378-238-14
16	501	80.4	375	4	US-09-451-501-14
17	501	80.4	375	4	US-09-451-501-19
18	501	80.4	375	4	US-09-451-501-21
19	501	80.4	375	4	US-09-451-501-23
20	501	80.4	375	4	US-09-451-501-27
21	501	80.4	376	2	US-08-525-596B-12
22	501	80.4	376	3	US-09-177-860A-12
23	501	80.4	376	3	US-08-891-789B-6
24	501	80.4	376	4	US-09-252-149B-27
25	501	80.4	376	4	US-09-252-149B-28
26	501	80.4	376	4	US-09-378-238-12
27	501	80.4	376	4	US-09-451-501-12

28	501	80.4	376	4	US-09-451-501-25	Sequence 25, Appl
29	500	80.3	375	4	US-09-252-149B-33	Sequence 33, Appl
30	495	79.5	375	4	US-09-252-149B-30	Sequence 30, Appl
31	490	78.7	375	3	US-08-891-789B-2	Sequence 2, Appl
32	490	78.7	375	4	US-09-252-149B-2	Sequence 2, Appl
33	490	78.7	375	4	US-09-252-149B-31	Sequence 31, Appl
34	468	75.1	374	4	US-09-252-149B-36	Sequence 36, Appl
35	468	75.1	374	4	US-09-378-238-29	Sequence 29, Appl
36	467	75.0	126	1	US-08-247-907A-2	Sequence 2, Appl
37	467	75.0	126	1	US-08-452-772-2	Sequence 2, Appl
38	467	75.0	126	2	US-08-765-875-4	Sequence 4, Appl
39	467	75.0	126	3	US-08-795-671-4	Sequence 4, Appl
40	467	75.0	126	4	US-09-414-234-2	Sequence 2, Appl
41	467	75.0	126	4	US-08-919-850-2	Sequence 2, Appl
42	467	75.0	126	5	PCR-US94-05288-2	Sequence 2, Appl
43	467	75.0	362	1	US-08-247-907A-11	Sequence 11, Appl
44	467	75.0	362	1	US-08-452-772-11	Sequence 11, Appl
45	467	75.0	362	4	US-09-414-234-11	Sequence 11, Appl

ALIGNMENTS

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RESULT 1
US-08-525-596B-6
: Sequence 6, Application US/08525596B
: Patient No. 5827733
: GENERAL INFORMATION:
: APPLICANT: Huynh, Thanh
: TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 4225 Executive Square, Suite 1400
: CITY: La Jolla
: STATE: CA
: COUNTRY: US
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: Windows95
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/525,596B
: FILING DATE: 19-SEP-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/07762
: FILING DATE: 08-JUL-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Wetherell, Jr., Ph.D., John R.
: REGISTRATION NUMBER: 31,678
: REFERENCE/DOCKET NUMBER: 07265/075001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-678-5070
: TELEFAX: 619-678-5099
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 126 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FRAGMENT TYPE: Internal
: US-08-525-596B-6

Query Match      80.4%; Score 501; DB 2; Length 126;
Best Local Similarity 80.7%; Pred. No. 6, 7e-52;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;
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1 DFGIDCDHEHTESSRCRCRYPLTVDEAFGWDMLAPKRYKANYCSGCECFNNVTFSWLR 60
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1. TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN

SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids

TYPE: amino acid

CURRENT APPLICATION NUMBER: US/09/378,238

US-08-525-596B-14

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? TOPLOGY: linear
? MOLECULE TYPE: protein
? FRAGMENT TYPE: internal
? SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-451-501-6
Query Match      80.4%; Score 501; DB 4; Length 126;
Best Local Similarity 80.7%; Pred. No. 6,7e-52;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;
OY   1 DFGLDCEHSTESRCRYPPLVDFEAFGWDIIAPKRYKANYSGCCFNNFTVSFWLRY 60
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Db    18 DFGLDCEHSTESRCRYPPLVDFEAFGWDIIAPKRYKANYSGCCF-----VFLOKY 72
OY   |
      |
Db    73 PHTHLVHOANPRGSAGPCTPTKMSPINMLTFNGKEQIITGKIIPAMVVDRCGCS 126

RESULT 5
US-09-378-238-21
Sequence 21, Application US/09378238
Patent No. 6465239
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
TITLE OF INVENTION: ACID AND PEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
FILE REFERENCE: JHU1120-9
CURRENT APPLICATION NUMBER: US/09/378, 238
CURRENT FILING DATE: 1999-08-19
EARLIER APPLICATION NUMBER: 08/795,071
EARLIER FILING DATE: 1997-02-05
EARLIER APPLICATION NUMBER: 08/525,596
EARLIER FILING DATE: 1995-10-25
EARLIER APPLICATION NUMBER: PCT/US94/03019
EARLIER FILING DATE: 1994-03-18
EARLIER APPLICATION NUMBER: 08/033,923
EARLIER FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 130
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-378-238-21
Query Match      80.4%; Score 501; DB 4; Length 130;
Best Local Similarity 80.7%; Pred. No. 7e-52;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;
OY   1 DFGLDCEHSTESRCRYPPLVDFEAFGWDIIAPKRYKANYSGCCFNNFTVSFWLRY 60
      |||||||
Db    22 DFGLDCEHSTESRCRYPPLVDFEAFGWDIIAPKRYKANYSGCCF-----VFLOKY 76
OY   61 PKVASHL-----BAGPCPTPKMSPINMLTFNGKEQIITGKIIPAMVVDRCGCS 109
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      |
Db    77 PHTHLVHOANPRGSAGPCTPTKMSPINMLTFNGKEQIITGKIIPAMVVDRCGCS 130

RESULT 6
US-09-378-238-19
Sequence 19, Application US/09378238
Patent No. 6465239
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
TITLE OF INVENTION: ACID AND PEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
FILE REFERENCE: JHU1120-9
CURRENT APPLICATION NUMBER: US/09/378, 238

? CURRENT FILING DATE: 1999-08-19
? EARLIER APPLICATION NUMBER: 08/795,071
? EARLIER FILING DATE: 1997-02-05
? EARLIER APPLICATION NUMBER: 08/525,596
? EARLIER FILING DATE: 1995-10-25
? EARLIER APPLICATION NUMBER: PCT/US94/03019
? EARLIER FILING DATE: 1994-03-18
? EARLIER APPLICATION NUMBER: 08/033,923
? EARLIER FILING DATE: 1993-03-19
? NUMBER OF SEQ ID NOS: 41
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 19
? LENGTH: 225
? TYPE: PRT
? ORGANISM: Gallus gallus
US-09-378-238-19
Query Match      80.4%; Score 501; DB 4; Length 225;
Best Local Similarity 80.7%; Pred. No. 1,4e-91;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;
OY   1 DFGLDCEHSTESRCRYPPLVDFEAFGWDIIAPKRYKANYSGCCFNNFTVSFWLRY 60
      |||||||
Db    117 DFGLDCEHSTESRCRYPPLVDFEAFGWDIIAPKRYKANYSGCCF-----VFLOKY 171
OY   61 PKVASHL-----BAGPCPTPKMSPINMLTFNGKEQIITGKIIPAMVVDRCGCS 109
      |
      |
Db    172 PHTHLVHOANPRGSAGPCTPTKMSPINMLTFNGKEQIITGKIIPAMVVDRCGCS 225

RESULT 7
US-08-525-596B-14
Sequence 14, Application US/08525596B
Patent No. 5827733
GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,596B
FILING DATE: 19-SEP-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07762
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D. John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 07265/075001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-525-596B-14

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Query Match	80.4%;	Score 501;	DB 2;	Length 375;
Best Local Similarity	-80.7%;	Pred. No. 2.5e-51;		
Matches 92;	Conservative 1;	Mismatches 11;	Indels 10;	Gaps 2;

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OY    1 DEGLDDEHSTESRCRRPLTVDFEAGWDMLIAPKRYANYCSGCECFNNFTVSFWLRY 60  
      |||||  
      |||||  
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      |||||  
  
Db   267 DEGLDDEHSTESRCRRPLTVDFEAGWDMILAKRKYANYSQSGCEF-----VFLQKY 321
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61 PKVSASHL-----EAGPCCPTPKNSPINMLFENGKEQIIIGKIPAMVYDRCGCS 109
 322 PHTHLVHQANPRGSGAPCCPTPKNSPINMLYFNGKEQIIIGKIPAMVYDRCGCS 375

RESULT 8
US-08-765-875-5
; Sequence 5, Application US/08765875
; Patent No. 5914234

APPLICANT: LEE, SE-JIN
APPLICANT: MCPHERRON, ALEXANDRA C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11

ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES

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; ZIP: 90067  
; COMPUTER READABLE FORM:  
; ADDITIONAL COMMENTS:
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.29
; CURRENT APPLICATION DATA:

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FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:
FILING DATE: 08-JUL-1994
APPLICATION NUMBER: US/08/2/2,163

TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: PD36411
; INVESTIGATION NUMBER: E-36/34/

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; SEQUENCE CHARACTERISTICS:
; INFORMATION FOR SEQ ID NO: 5

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STRANDEDNESS: single
TOPOLOGY: linear

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CLONE: GDF-8
FEATURE:
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US-08-765-875-5

Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2

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Db      267  DFGLDCEHSTESKCRYP LTVDFEAFGMDWITAPKRYANYSCECF-----VFLOKY 321
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QY 61 PKVSASHL-----EAGPCTPTKNSPINMLFNGKEQIITGKIPAMVVDRCGCS 109
 | | | | |
Db 322 PHTHLVHQANPRGSAGPCCTPTKNSPINMLFYNGKEQIITGKIPAMVVDRCGCS 375

RESULT 9
US-08-795-671-5
; Sequence 5, Application US/08795671
Data No. 600843

APPLICANT: Se-Jin Lee and Alexandra McPherron
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
NUMBER OF SEQUENCES: 9

ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla

COONIKI: 05
ZIP: 92037
COMPUTER READABLE FORM:

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; COME ON: IBM PC COMPATIBLE
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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CLASSIFICATION: 800

REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/106001

TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; IMMEDIATE SOURCE:
; CLONE: GDF-8
; FEATURE:

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LOCATION: 1..3/3
US-08-795-671-5

best local similarity 80.78
Matches 92; Conservative

Db 267 DEGLDCDEHSTESRCCRYPLT

Db 322 PHTHLVHQANPRGSAGPCCTP

US-09-177-860A-14
; Sequence 14, Application US/0

APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin

CORRESPONDENCE ADDRESS:

ADDRESS: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: US
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,860A
FILING DATE: 23-OCT-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/525,596
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/075003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-677-1456
TELEFAX: 858-677-1465
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-177-860A-14

Query Match 80.4%; Score 501; DB 3; Length 375;
Best Local Similarity 80.7%; Pred. No. 2.5e-51;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

1 DFGLCDDEHSTESRCRCRPLTVDFEAFGMDWIIAPKRYKANYCSGCECFNNFTVSFMLRV 60
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267 DFGLCDDEHSTESRCRCRPLTVDFEAFGMDWIIAPKRYKANYCSGCECF-----VFLQKY 321

QY 61 PKVSASHL-----EAGPCCPTPKMSPIINMLYFNKGEQIITGKIPAMVVDRCGS 109
|
DB 322 PHTHLVHOANPRGSAGPCCPTPKMSPIINMLYFNKGEQIITGKIPAMVVDRCGS 375

RESULT 11
US-09-252-149B-29
; Sequence 29, Application US/09252149B
; Patent No. 6369201
; GENERAL INFORMATION:
; APPLICANT: Barker, Christopher A.
; APPLICANT: Morsey, Mohamed
; TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
; FILE REFERENCE: 9001-0042
; CURRENT APPLICATION NUMBER: US/09/252,149B
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/075,213
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-252-149B-29

Query Match 80.4%; Score 501; DB 4; Length 375;
Best Local Similarity 80.7%; Pred. No. 2.5e-51;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 1 DFGLCDDEHSTESRCRCRPLTVDFEAFGMDWIIAPKRYKANYCSGCECFNNFTVSFMLRV 60
|||||
DB 267 DFGLCDDEHSTESRCRCRPLTVDFEAFGMDWIIAPKRYKANYCSGCECF-----VFLQKY 321

QY 61 PKVSASHL-----EAGPCCPTPKMSPIINMLYFNKGEQIITGKIPAMVVDRCGS 109
|
DB 322 PHTHLVHOANPRGSAGPCCPTPKMSPIINMLYFNKGEQIITGKIPAMVVDRCGS 375

RESULT 12
US-09-252-149B-32
; Sequence 32, Application US/09252149B
; Patent No. 6369201
; GENERAL INFORMATION:
; APPLICANT: Barker, Christopher A.
; APPLICANT: Morsey, Mohamed
; TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
; FILE REFERENCE: 9001-0042
; CURRENT APPLICATION NUMBER: US/09/252,149B
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/075,213
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-252-149B-32

Query Match 80.4%; Score 501; DB 4; Length 375;
Best Local Similarity 80.7%; Pred. No. 2.5e-51;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

1 DFGLCDDEHSTESRCRCRPLTVDFEAFGMDWIIAPKRYKANYCSGCECFNNFTVSFMLRV 60
|||||
267 DFGLCDDEHSTESRCRCRPLTVDFEAFGMDWIIAPKRYKANYCSGCECF-----VFLQKY 321

QY 61 PKVSASHL-----EAGPCCPTPKMSPIINMLYFNKGEQIITGKIPAMVVDRCGS 109
|
DB 322 PHTHLVHOANPRGSAGPCCPTPKMSPIINMLYFNKGEQIITGKIPAMVVDRCGS 375

RESULT 13
US-09-252-149B-34
; Sequence 34, Application US/09252149B
; Patent No. 6369201
; GENERAL INFORMATION:
; APPLICANT: Barker, Christopher A.
; APPLICANT: Morsey, Mohamed
; TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
; FILE REFERENCE: 9001-0042
; CURRENT APPLICATION NUMBER: US/09/252,149B
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/075,213
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-252-149B-34

Query Match 80.4%; Score 501; DB 4; Length 375;
Best Local Similarity 80.7%; Pred. No. 2.5e-51;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

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|||||
267 DFGLCDDEHSTESRCRCRPLTVDFEAFGMDWIIAPKRYKANYCSGCECF-----VFLQKY 321

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OM protein - protein search, using sw model

Run on: March 25, 2003, 15:12:24 ; Search time 14 Seconds
(without alignments) 416.242 Million cell updates/sec

Title: US-09-620-586B-19

Perfect score: 623

Sequence: 1 DFGDCEHSTESRCRYPL.....KEQIITYGKIPAMVYDRGCS 109

Scoring table:

BLASTSUM62
Gapop.10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubppaa/PCIT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubppaa/PCITUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501	80.4	126	9 US-09-859-211-6	Sequence 6, Appl1
2	501	80.4	130	9 US-09-859-211-33	Sequence 33, Appl1
3	501	80.4	226	9 US-09-859-211-35	Sequence 8, Appl1
4	501	80.4	374	9 US-09-841-730-8	Sequence 2, Appl1
5	501	80.4	375	9 US-09-841-730-2	Sequence 14, Appl1
6	501	80.4	375	9 US-09-841-730-14	Sequence 18, Appl1
7	501	80.4	375	9 US-09-841-730-18	Sequence 23, Appl1
8	501	80.4	375	9 US-09-859-211-14	Sequence 14, Appl1
9	501	80.4	375	9 US-09-859-211-23	Sequence 27, Appl1
10	501	80.4	375	9 US-09-859-211-27	Sequence 29, Appl1
11	501	80.4	375	9 US-09-859-211-29	Sequence 5, Appl1
12	501	80.4	375	10 US-09-454-540-5	Sequence 4, Appl1
13	501	80.4	376	9 US-09-841-730-4	Sequence 6, Appl1
14	501	80.4	376	9 US-09-841-730-6	Sequence 12, Appl1
15	501	80.4	376	9 US-09-859-211-12	Sequence 25, Appl1
16	501	80.4	376	9 US-09-859-211-25	Sequence 38, Appl1
17	501	80.4	376	9 US-09-813-398-38	Sequence 11, Appl1
18	501	80.4	376	10 US-09-859-894A-11	Sequence 16, Appl1
19	500	80.3	375	9 US-09-841-730-16	

20	500	80.3	375	9 US-09-859-211-31	Sequence 31, Appl1
21	496	79.6	375	10 US-09-859-894A-5	Sequence 5, Appl1
22	495	79.5	375	9 US-09-841-730-10	Sequence 10, Appl1
23	495	79.5	375	9 US-09-859-211-19	Sequence 19, Appl1
24	494	79.3	109	10 US-09-754-826-2	Sequence 2, Appl1
25	490	78.7	375	9 US-09-841-730-12	Sequence 12, Appl1
26	490	78.7	375	9 US-09-859-211-21	Sequence 21, Appl1
27	468	75.1	374	9 US-09-841-730-20	Sequence 20, Appl1
28	467	75.0	126	10 US-09-454-540-4	Sequence 4, Appl1
29	467	75.0	126	10 US-09-859-894A-4	Sequence 4, Appl1
30	467	75.0	407	9 US-09-841-730-25	Sequence 25, Appl1
31	467	75.0	407	10 US-09-454-540-2	Sequence 2, Appl1
32	467	75.0	407	10 US-09-454-540-6	Sequence 6, Appl1
33	467	75.0	407	10 US-09-813-398-33	Sequence 2, Appl1
34	467	75.0	408	9 US-09-813-398-33	Sequence 33, Appl1
35	463	74.3	136	9 US-09-841-730-29	Sequence 29, Appl1
36	463	74.3	157	9 US-09-841-730-27	Sequence 27, Appl1
37	462	74.2	108	9 US-09-859-211-8	Sequence 8, Appl1
38	402.5	64.6	128	10 US-09-205-658-317	Sequence 317, App
39	218	35.0	120	10 US-09-813-459-20	Sequence 20, Appl1
40	218	35.0	120	12 US-10-115-406-20	Sequence 20, Appl1
41	218	35.0	121	9 US-09-859-211-46	Sequence 46, Appl1
42	218	35.0	121	9 US-09-880-708-24	Sequence 24, Appl1
43	218	35.0	408	9 US-09-813-398-20	Sequence 20, Appl1
44	218	35.0	408	9 US-09-813-398-22	Sequence 22, Appl1
45	216.5	34.8	352	8 US-08-981-490B-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1

US-09-859-211-6
Sequence 6, Application US/09859211
Patent No. US20020157125A1
GENERAL INFORMATION:
APPLICANT: McPherson, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/144001
CURRENT APPLICATION NUMBER: US/09/859, 211
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/019, 070
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 08/862, 445
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 08/847, 910
PRIOR FILING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: 08/795, 071
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: 08/525, 596
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: PCT/US94/03019
PRIOR FILING DATE: 1994-03-18
PRIOR APPLICATION NUMBER: 08/033, 923
PRIOR FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 126
TYPE: PRT
ORGANISM: Mus musculus
US-09-859-211-6

Query Match 80.4%; Score 501; DB 9; Length 126;
Best Local Similarity 80.7%; Pred. No. 1.7e-43;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 1 DFGDCEHSTESRCRYPLTVDPPEARAGWMDIAPKRYKANYSGGCEENFTVSMARY 60
DB 18 DFGDCEHSTESRCRYPLTVDPPEARAGWMDIAPKRYKANYSGGCEP-----VFLQRT 72
QY 61 PKYASHL-----EAGPCCTPTKMSPIINMLYFNGKEQIIGKIPAMVYDRGCS 109

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Db      73 PHTHLVHQANPRGSAGPCTPTPKMSPINMLYFNKGKEQIITYGKIIPAMVVDRCGCS 126
       |-----|
       |
RESULT 2
US-09-859-211-33
; Sequence 33, Application US/09859211
; Patent No. US20020157125A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/144001
CURRENT APPLICATION NUMBER: US/09/859, 211
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/019, 070
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 08/862, 445
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 08/847, 910
PRIOR FILING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: 08/795, 071
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: 08/525, 596
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: PCT/US94/03019
PRIOR FILING DATE: 1994-03-18

Db      77 PHTHLVHOANPRGSAGPCTPTPKMSPINMLYFNKGKEQIITYGKIIPAMVVDRCGCS 130
       |-----|
       |
Query Match          80.4%; Score 501; DB 9; Length 130;
Best Local Similarity 80.7%; Fred. 1.7e-43;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2.

Oy      1 DFGLCDSEHSTSRCCRPILVDFEAFGDMWTIARKRYKANCSCGEFNNFTVSFWLRY 60
       |-----|
Db      22 DEGLDCDEHSTSRCCRPILVDFEAFGDMWTIARKRYKANCSCGECE-----VFLOKY 76
       |-----|
Oy      61 PKVASHL-----EAGPCCTPTXMSPINMLYFNKGKEQIITYGKIIPAMVVDRCGCS 109
       |-----|
Db      77 PHTHLVHOANPRGSAGPCTPTPKMSPINMLYFNKGKEQIITYGKIIPAMVVDRCGCS 130
       |-----|
       |
RESULT 3
US-09-859-211-35
; Sequence 35, Application US/09859211
; Patent No. US20020157125A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/144001
CURRENT APPLICATION NUMBER: US/09/859, 211
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/019, 070
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 08/862, 445
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 08/847, 910
PRIOR FILING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: 08/795, 071
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: 08/525, 596
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: PCT/US94/03019
PRIOR FILING DATE: 1994-03-18

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P R I O R   A P P L I C A T I O N   N U M B E R : 08/033,923
P R I O R   F I L I N G   D A T E : 1993-03-19
N U M B E R   O F   S E Q   I D   N O S : 51
S O F T W A R E : F a s t S e q   f o r   W i n d o w s   V e r s i o n   4 . 0
S E Q   I D   N O   35
L E N G T H : 226
T Y P E : P R T
O R G A N I S M : G a l l u s   g a l l u s
U S - 09-859-211-35

Q u e r y   M a t c h
B e s t   L o c a l   S i m i l a r i t y   80.4%;   S c o r e   501;   D B   9;   L e n g t h   226;
M a t c h e s   92;   C o n s e r v a t i v e   1;   M i s m a t c h e s   11;   I n d e l s   10;   G a p s   2;

O Y      1   D F G I D C D E H S T E S C C R P L T V D P E A R G W M I I A P K R Y K A N Y S G C E F N N T V S F W L R V   60
D b      118   D F G I D C D E H S T E S C C R P L T V D P E A R G W M I I A P K R Y K A N Y S G C E F -----V F L O K Y   172

O Y      61   P K V A S H L -----E A G P C C T P T K M S P I N M L Y F N G K E Q I I Y G K I P A M V V D R C G S   109
D b      173   P H T H L V H Q A N D R G S A G P C C T P T K M S P I N M L Y F N G K E Q I I Y G K I P A M V V D R C G S   226

R E S U L T   4
U S - 09-841-730-8
; S e q u e n c e   8 ,   A p p l i c a t i o n   U S / 09841730
; P a t e n t   N o .   U S 20020157126A1
; G E N E R A L   I N F O R M A T I O N :
; A P P L I C A N T : L e e , S e - J i n
; T I T L E   O F   I N V E N T I O N : G R O W T H   D I F F E R E N T I A T I O N   F A C T O R   R E C E P T O R S ,
; F I L E   R E F E R E N C E : J H 01470-2
; C U R R E N T   A P P L I C A T I O N   N U M B E R : U S / 09/841,730
; C U R R E N T   F I L I N G   D A T E : 2001-04-24
; P R I O R   A P P L I C A T I O N   N U M B E R : 09/626,896
; P R I O R   F I L I N G   D A T E : 2000-07-27
; P R I O R   A P P L I C A T I O N   N U M B E R : 09/485,046
; P R I O R   F I L I N G   D A T E : 2000-01-31
; P R I O R   A P P L I C A T I O N   N U M B E R : P C T / U S 98 / 15598
; P R I O R   F I L I N G   D A T E : 1998-07-28
; P R I O R   A P P L I C A T I O N   N U M B E R : 60/054,461
; P R I O R   F I L I N G   D A T E : 1997-08-01
; N U M B E R   O F   S E Q   I D   N O S : 29
; S O F T W A R E : F a s t S e q   f o r   W i n d o w s   V e r s i o n   4 . 0
; S E Q   I D   N O   8
; L E N G T H : 374
; T Y P E : P R T
; O R G A N I S M : G a l l u s   g a l l u s
U S - 09-841-730-8

Q u e r y   M a t c h
B e s t   L o c a l   S i m i l a r i t y   80.4%;   S c o r e   501;   D B   9;   L e n g t h   374;
M a t c h e s   92;   C o n s e r v a t i v e   1;   M i s m a t c h e s   11;   I n d e l s   10;   G a p s   2;

O Y      1   D F G I D C D E H S T E S C C R P L T V D P E A R G W M I I A P K R Y K A N Y S G C E F N N T V S F W L R V   60
D b      266   D F G I D C D E H S T E S C C R P L T V D P E A R G W M I I A P K R Y K A N Y S G C E F -----V F L O K Y   320

O Y      61   P K V A S H L -----E A G P C C T P T K M S P I N M L Y F N G K E Q I I Y G K I P A M V V D R C G S   109
D b      321   P H T H L V H Q A N D R G S A G P C C T P T K M S P I N M L Y F N G K E Q I I Y G K I P A M V V D R C G S   374

R E S U L T   5
U S - 09-841-730-2
; S e q u e n c e   2 ,   A p p l i c a t i o n   U S / 09841730
; P a t e n t   N o .   U S 20020157126A1
; G E N E R A L   I N F O R M A T I O N :
; A P P L I C A N T : L e e , S e - J i n
; A P P L I C A N T : M c H e r r o n , A l e x a n d r a   C .
; T I T L E   O F   I N V E N T I O N : G R O W T H   D I F F E R E N T I A T I O N   F A C T O R   R E C E P T O R S ,
; F I L E   O F   I N V E N T I O N : A G O N I S T S   A N D   A N T A G O N I S T S   T H E R E O F ,   A N D   M E T H O D S   O F   U S I N G   S A M E

```



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FILE REFERENCE: JH01470-2
CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/626,896
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 2
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-09-841-730-2
```

```
Query Match
Best Local Similarity 80.4%; Score 501; DB 9; Length 375;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;
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QY 1 DEGLDDEHSTESRCCRYPLTVDEAFGMDMIIAPRRYKANYCSECEFNFTVSEFLRV 60
DB 267 DFGLDDEHSTESRCCRYPLTVDEAFGMDMIIAPRRYKANYCSECEFNFTVSEFLRV 60
QY 61 PKVSASHL-----EAGPCCTPTKMSPIINMLYFNGKEQIIGKIPAMVYDRCGCS 109
DB 322 PHTHLVHQANPRGSAGPCTPTKMSPIINMLYFNGKEQIIGKIPAMVYDRCGCS 375
```

```
RESULT 6
US-09-841-730-14
Sequence 14, Application US/09841730
Patent No. US20020157126A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
FILE REFERENCE: JH01470-2
CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/626,896
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 14
LENGTH: 375
TYPE: PRT
ORGANISM: Porcine
US-09-841-730-14
```

```
Query Match
Best Local Similarity 80.4%; Score 501; DB 9; Length 375;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;
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```
QY 1 DEGLDDEHSTESRCCRYPLTVDEAFGMDMIIAPRRYKANYCSECEFNFTVSEFLRV 60
DB 267 DFGLDDEHSTESRCCRYPLTVDEAFGMDMIIAPRRYKANYCSECEFNFTVSEFLRV 60
QY 61 PKVSASHL-----EAGPCCTPTKMSPIINMLYFNGKEQIIGKIPAMVYDRCGCS 109
DB 322 PHTHLVHQANPRGSAGPCTPTKMSPIINMLYFNGKEQIIGKIPAMVYDRCGCS 375
```

```
RESULT 7
US-09-841-730-18
Sequence 18, Application US/09841730
Patent No. US20020157126A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
FILE REFERENCE: JH01470-2
CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/626,896
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 18
LENGTH: 375
TYPE: PRT
ORGANISM: Melagris gallapavo
US-09-841-730-18
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Query Match
Best Local Similarity 80.4%; Score 501; DB 9; Length 375;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;
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QY 1 DEGLDDEHSTESRCCRYPLTVDEAFGMDMIIAPRRYKANYCSECEFNFTVSEFLRV 60
DB 267 DFGLDDEHSTESRCCRYPLTVDEAFGMDMIIAPRRYKANYCSECEFNFTVSEFLRV 60
QY 61 PKVSASHL-----EAGPCCTPTKMSPIINMLYFNGKEQIIGKIPAMVYDRCGCS 109
DB 322 PHTHLVHQANPRGSAGPCTPTKMSPIINMLYFNGKEQIIGKIPAMVYDRCGCS 375
```

```
RESULT 8
US-09-859-211-14
Sequence 14, Application US/09859211
Patent No. US20020157125A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/144001
CURRENT APPLICATION NUMBER: US/09/859,211
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/019,070
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 08/862,445
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR FILING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: 08/795,071
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: 08/525,596
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: PCT/US94/03019
PRIOR FILING DATE: 1994-03-18
PRIOR APPLICATION NUMBER: 08/033,923
PRIOR FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 14
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-09-859-211-14
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Query Match      80.4%; Score 501; DB 9; Length 375;
Best Local Similarity 80.7%; Pred. No. 4,9e-43;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DGLDGDHSTESRCRYPITVDPEAFGMDWIIAPKRYKANYSCECEFNFTVSFWLRY 60
    |||||||
DB 267 DGLDGDHSTESRCRYPITVDPEAFGMDWIIAPKRYKANYSCECEFNFTVSFWLRY 60
    |||||||
OY 61 PKVASHL-----EAGPCPTPKMSPINMLYFNGKEQIITGKIPAMVYDRGCS 109
    |||||||
DB 322 PTHLVHQANPRGSAGPCPTPKMSPINMLYFNGKEQIITGKIPAMVYDRGCS 375

RESULT 9
US-09-859-211-23
; Sequence 23, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-859-211-23

Query Match      80.4%; Score 501; DB 9; Length 375;
Best Local Similarity 80.7%; Pred. No. 4,9e-43;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DGLDGDHSTESRCRYPITVDPEAFGMDWIIAPKRYKANYSCECEFNFTVSFWLRY 60
    |||||||
DB 267 DGLDGDHSTESRCRYPITVDPEAFGMDWIIAPKRYKANYSCECEFNFTVSFWLRY 60
    |||||||
OY 61 PKVASHL-----EAGPCPTPKMSPINMLYFNGKEQIITGKIPAMVYDRGCS 109
    |||||||
DB 322 PTHLVHQANPRGSAGPCPTPKMSPINMLYFNGKEQIITGKIPAMVYDRGCS 375

RESULT 10
US-09-859-211-27
; Sequence 27, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US/09/859,211
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Meleagris gallopavo
US-09-859-211-27

Query Match      80.4%; Score 501; DB 9; Length 375;
Best Local Similarity 80.7%; Pred. No. 4,9e-43;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DGLDGDHSTESRCRYPITVDPEAFGMDWIIAPKRYKANYSCECEFNFTVSFWLRY 60
    |||||||
DB 267 DGLDGDHSTESRCRYPITVDPEAFGMDWIIAPKRYKANYSCECEFNFTVSFWLRY 60
    |||||||
OY 61 PKVASHL-----EAGPCPTPKMSPINMLYFNGKEQIITGKIPAMVYDRGCS 109
    |||||||
DB 322 PTHLVHQANPRGSAGPCPTPKMSPINMLYFNGKEQIITGKIPAMVYDRGCS 375

RESULT 11
US-09-859-211-29
; Sequence 29, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US/09/859,211
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Porcine
US-09-859-211-29

Query Match      80.4%; Score 501; DB 9; Length 375;
Best Local Similarity 80.7%; Pred. No. 4,9e-43;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DGLDGDHSTESRCRYPITVDPEAFGMDWIIAPKRYKANYSCECEFNFTVSFWLRY 60
    |||||||
DB 267 DGLDGDHSTESRCRYPITVDPEAFGMDWIIAPKRYKANYSCECEFNFTVSFWLRY 60
    |||||||
OY 61 PKVASHL-----EAGPCPTPKMSPINMLYFNGKEQIITGKIPAMVYDRGCS 109
    |||||||
DB 322 PTHLVHQANPRGSAGPCPTPKMSPINMLYFNGKEQIITGKIPAMVYDRGCS 375
```

OY 61 PKVSASHL-----EAGPCTPTKMSPINMLYFNGKEQIIYGIKIPAMVYDRGCS 109
 Db 322 PHTHLVHOANPRGSAGPCTPTKMSPINMLYFNGKEQIIYGIKIPAMVYDRGCS 375

RESULT 12

US-09-454-540-5
 ; Sequence 5, Application US/09454540
 ; Patent No. US2001005358A1

GENERAL INFORMATION:

APPLICANT: Se-jin Lee and Alexandra McPherron
 TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: California
 COUNTRY: US
 ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/454,540
 FILING DATE: 06-DEC-1999
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/795,671
 FILING DATE: February 6, 1997
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: HATLE, PH.D., LISA A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07265/106001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 375 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 IMMEDIATE SOURCE:
 CLONE: GDF-8
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..375
 US-09-454-540-5

Query Match 80.4%; Score 501; DB 10; Length 375;
 Best Local Similarity 80.7%; Pred. No. 4.9e-43;
 Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGIDCDHSTESRCRCRYPLTVDFEAFGWDIIAPKRYKANYCGEGEENFTVSFMLRV 60
 Db 267 DFGIDCDHSTESRCRCRYPLTVDFEAFGWDIIAPKRYKANYCGEGEENFTVSFMLRV 60
 OY 61 PKVSASHL-----EAGPCTPTKMSPINMLYFNGKEQIIYGIKIPAMVYDRGCS 109
 Db 322 PHTHLVHOANPRGSAGPCTPTKMSPINMLYFNGKEQIIYGIKIPAMVYDRGCS 375

RESULT 13
 US-09-841-730-4
 ; Sequence 4, Application US/09841730
 ; Patent No. US20020157126A1
 ; GENERAL INFORMATION:

APPLICANT: Lee, Se-jin
 TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
 AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
 FILE REFERENCE: JHU1470-2
 CURRENT APPLICATION NUMBER: US/09/841,730
 PRIOR FILING DATE: 2001-04-24
 PRIOR APPLICATION NUMBER: 09/626,896
 PRIOR FILING DATE: 2000-07-27
 PRIOR APPLICATION NUMBER: 09/485,046
 PRIOR FILING DATE: 2000-01-31
 PRIOR APPLICATION NUMBER: PCT/US98/15598
 PRIOR FILING DATE: 1998-07-28
 PRIOR APPLICATION NUMBER: 60/054,461
 PRIOR FILING DATE: 1997-08-01
 NUMBER OF SEQ ID NOS: 29
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 4
 LENGTH: 376
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-841-730-4

Query Match 80.4%; Score 501; DB 9; Length 376;
 Best Local Similarity 80.7%; Pred. No. 4.9e-43;
 Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGIDCDHSTESRCRCRYPLTVDFEAFGWDIIAPKRYKANYCGEGEENFTVSFMLRV 60
 Db 268 DFGIDCDHSTESRCRCRYPLTVDFEAFGWDIIAPKRYKANYCGEGEENFTVSFMLRV 60
 OY 61 PKVSASHL-----EAGPCTPTKMSPINMLYFNGKEQIIYGIKIPAMVYDRGCS 109
 Db 323 PHTHLVHOANPRGSAGPCTPTKMSPINMLYFNGKEQIIYGIKIPAMVYDRGCS 376

RESULT 14
 US-09-841-730-6
 ; Sequence 6, Application US/09841730
 ; Patent No. US20020157126A1
 ; GENERAL INFORMATION:
 APPLICANT: Lee, Se-jin
 TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
 AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
 FILE REFERENCE: JHU1470-2
 CURRENT APPLICATION NUMBER: US/09/841,730
 PRIOR FILING DATE: 2001-04-24
 PRIOR APPLICATION NUMBER: 09/626,896
 PRIOR FILING DATE: 2000-07-27
 PRIOR APPLICATION NUMBER: 09/485,046
 PRIOR FILING DATE: 2000-01-31
 PRIOR APPLICATION NUMBER: PCT/US98/15598
 PRIOR FILING DATE: 1998-07-28
 PRIOR APPLICATION NUMBER: 60/054,461
 PRIOR FILING DATE: 1997-08-01
 NUMBER OF SEQ ID NOS: 29
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 6
 LENGTH: 376
 TYPE: PRT
 ORGANISM: Rattus norvegicus
 US-09-841-730-6

Query Match 80.4%; Score 501; DB 9; Length 376;
 Best Local Similarity 80.7%; Pred. No. 4.9e-43;
 Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGIDCDHSTESRCRCRYPLTVDFEAFGWDIIAPKRYKANYCGEGEENFTVSFMLRV 60
 Db 268 DFGIDCDHSTESRCRCRYPLTVDFEAFGWDIIAPKRYKANYCGEGEENFTVSFMLRV 60
 OY 61 PKVSASHL-----EAGPCTPTKMSPINMLYFNGKEQIIYGIKIPAMVYDRGCS 109

Db 323 PHTHLVHQANPRGSAGPCTPTKMSPINMLYFNGKEQIITYGKIPAMVVDRCGCS 376

RESULT 15
US-09-859-211-12

; Sequence 12, Application US/09859211
; Patent No. US20020157125A1

; GENERAL INFORMATION:

; APPLICANT: Lee, Se-Jin

; APPLICANT: McPherron, Alexandra C.

; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8

; FILE REFERENCE: 07265/144001

; CURRENT FILING DATE: 2001-05-15

; PRIOR APPLICATION NUMBER: US/09/859, 211

; PRIOR FILING DATE: 1998-02-05

; PRIOR APPLICATION NUMBER: 08/862,445

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 08/847,910

; PRIOR FILING DATE: 1997-04-28

; PRIOR APPLICATION NUMBER: 08/795,071

; PRIOR FILING DATE: 1997-02-05

; PRIOR APPLICATION NUMBER: 08/525,596

; PRIOR FILING DATE: 1995-10-26

; PRIOR APPLICATION NUMBER: PCT/US94/03019

; PRIOR FILING DATE: 1994-03-18

; PRIOR APPLICATION NUMBER: 08/033,923

; PRIOR FILING DATE: 1993-03-19

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 376

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-859-211-12

Query Match 80.4%; Score 501; DB 9; Length 376;
Best Local Similarity 80.7%; Pred. No. 4.9e-43;

Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 1 DGLDDEHSTESRCRPLTVDFEAFGMDWTIAPKRYKANYGSGECEFNNFTYSFWLRV 60

Db 268 DGLDDEHSTESRCRPLTVDFEAFGMDWTIAPKRYKANYGSGECEF-----VFLQKY 322

QY 61 PVSASHL-----EAGPCTPTKMSPINMLYFNGKEQIITYGKIPAMVVDRCGCS 109

Db 323 PHTHLVHQANPRGSAGPCTPTKMSPINMLYFNGKEQIITYGKIPAMVVDRCGCS 376

Search completed: March 25, 2003, 15:17:30
Job time : 14 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 25, 2003, 15:02:48 ; Search time 72 Seconds
(without alignments)
201.727 Million cell updates/sec

Title: US-09-620-586B-19

Perfect score: 623

Sequence: 1 DFGLDCEHSTESRCRYPL.....KEQIIYKIPAMVYDRGCS 109

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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2: /SIDs2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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22: /SIDs2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SIDs2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	623	100.0	109	22	AAB20149
2	530.5	85.2	254	22	AAB20152
3	504	80.9	375	20	AAB33845
4	501	80.4	109	22	AAB20141
5	501	80.4	109	23	AA651935
6	501	80.4	126	15	AA663161
7	501	80.4	126	19	AA669883
8	501	80.4	126	20	AA669885
9	501	80.4	126	22	AA673182
10	501	80.4	130	22	AA673189

11	501	80.4	160	22	AAB20153	Growth differentiat
12	501	80.4	226	22	AA673188	Chicken GDF-8. Ga
13	501	80.4	362	22	AAB20132	Turkey growth diff
14	501	80.4	374	23	AAU75633	Chicken promyostat
15	501	80.4	375	15	AA663160	Human growth diff
16	501	80.4	375	19	AA669888	Chicken growth dif
17	501	80.4	375	19	AA669891	Pig growth differe
18	501	80.4	375	19	AA669885	Human growth diff
19	501	80.4	375	19	AA665460	Human growth diffe
20	501	80.4	375	20	AA633838	Amino acid sequenc
21	501	80.4	375	20	AA633839	Amino acid sequenc
22	501	80.4	375	20	AA633840	Amino acid sequenc
23	501	80.4	375	20	AA633841	Amino acid sequenc
24	501	80.4	375	20	AA633843	Amino acid sequenc
25	501	80.4	375	20	AA633844	Amino acid sequenc
26	501	80.4	375	20	AA633937	Amino acid sequenc
27	501	80.4	375	20	AA633938	Amino acid sequenc
28	501	80.4	375	20	AA633932	Amino acid sequenc
29	501	80.4	375	20	AA633935	Amino acid sequenc
30	501	80.4	375	20	AA631189	Human GDF-8 protei
31	501	80.4	375	20	AA631192	Chicken GDF-8 prot
32	501	80.4	375	20	AA631194	Turkey GDF-8 prote
33	501	80.4	375	20	AA697887	Human myostatin.
34	501	80.4	375	21	AAB21087	Human GDF-8. Homo
35	501	80.4	375	21	AA692035	Human growth diffe
36	501	80.4	375	21	AA677566	Human growth diffe
37	501	80.4	375	22	AAB73187	Human GDF-8 #2. H
38	501	80.4	375	22	AAB20131	Human growth diffe
39	501	80.4	375	22	AAB20133	Chicken growth diffe
40	501	80.4	375	22	AAB20138	Pig growth differe
41	501	80.4	375	23	AA618659	Human promyostat
42	501	80.4	375	23	AA618662	Chicken promyostat
43	501	80.4	375	23	AA618665	Porcine promyostat
44	501	80.4	375	23	AA618667	Meleagris gallopav
45	501	80.4	375	23	AAU75620	Human promyostat

ALIGNMENTS

RESULT 1	
AA620149	
ID	AA620149 standard; Protein: 109 AA.
AC	AA620149;
XX	
DT	30-APR-2001 (first entry)
XX	
DE	Growth differentiation factor 8 AutoVac construct GDF-8 p30-2.
XX	
KW	Growth differentiation factor 8; GDF-8; myostatin; tetanus toxin;
KW	T-cell epitope; down-regulation; vaccine; muscle; meat; cachexia;
KW	cardiant; human; mutant; mutein.
XX	
OS	Chimeric - Homo sapiens.
OS	Chimeric - Clostridium tetani.
OS	Synthetic.
XX	
FT	Key
FT	Location/Qualifiers
FT	1..48
FT	/note= "identical to residues 267-314 of human
FT	GDF-8"
FT	Region
FT	49..69
FT	/note= "tetanus toxoid p2 epitope"
FT	Region
FT	70..109
FT	/note= "identical to residues 336-375 of human
FT	GDF-8"
FT	Misc-difference 73
FT	/note= "Cys-73 may be substituted by Ser to avoid
FT	disulfide bond formation"
FT	Misc-difference 90..91
FT	/note= "optionally replaced by Glu-Gly"
XX	

```
PN WO200105820-A2.
XX
XX 25-JAN-2001.
PD
XX 20-JUL-2000; 2000WO-DK00413.
PF
XX 20-JUL-1999; 99DK-0001014.
PR 26-JUL-1999; 99US-0145275.
XX
XX (MEBI-) M & E BIOTECH AS.
XX
XX Halkier T, Mouritsen S, Klysner S.
PI WPI: 2001-112680/12.
DR
XX
XX Increasing the muscle mass of animals used in meat production by down
PT regulating growth differentiation factor 8 (GDF-8) activity in the
PT animal through induction of anti-GDF-8 antibody production -
XX
XX Example 1; Page 101-102; 110pp; English.
PS
XX
XX The present sequence is that of AutoVac construct GDF-8 P30-2,
CC comprising the 109 C-terminal amino acid residues of human
CC growth differentiation factor 8 (GDF-8) in which residues 49-69 are
CC replaced by the promiscuous tetanus toxin T-cell epitope P30 (see
CC AAB20144). It is an object of the invention to produce a
CC recombinant therapeutic vaccine that is capable of effecting
CC down-regulation of GDF-8 in order to increase the muscle growth
CC rate of farm animals. The vaccines (see AAB20145-53) are capable
CC of breaking autotolerance against autologous GDF-8. They comprise
CC the C-terminal portion of human GDF-8 in which a portion of the
CC native sequence is replaced by a T-cell epitope such as P30, with
CC minimal disturbance of the authentic 3-dimensional structure of
CC the protein. Nucleic acids encoding the GDF-8 variants can be used
CC for genetic immunisation of the animals. Down-regulation of GDF-8
CC activity can increase muscle mass by up to at least 45% in cattle,
CC pigs and poultry used for meat production, reducing the need for
CC antibiotic feed-additives. Anti-GDF8 vaccines can be used to
CC treat human diseases such as cancer cachexia where muscle atrophy is
CC pronounced and for patients suffering from acute and chronic heart
CC failure.
CC
XX Sequence 109 AA;
SQ
Query Match 100.0%; Score 623; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 3,2e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFGIDCDDEHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANYGSGCEFFNFTVSFWLRY 60
DB 1 DFGIDCDDEHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANYGSGCEFFNFTVSFWLRY 60
QY 61 PKVSASHLEAGPCCPTPKMSPINMLYFNKGKQIILYKIPAMVYDRGCGS 109
DB 61 PKVSASHLEAGPCCPTPKMSPINMLYFNKGKQIILYKIPAMVYDRGCGS 109
RESULT 2
AAB20152
ID AAB20152 standard; Protein; 254 AA.
XX
XX AAB20152;
AC
XX
XX 30-APR-2001 (first entry)
DT
XX
XX Growth differentiation factor 8 AutoVac construct GDF-8 dimer.
DE
XX
XX Growth differentiation factor 8; GDF-8; myostatin; tetanus toxin;
KM T-cell epitope; down-regulation; vaccine; muscle; meat; cachexia;
KW cardiant; human; mutant; mulein.
XX
XX Chimeric - Homo sapiens.
OS Chimeric - Clostridium tetani.
```

```
OS Synthetic.
FH Key Location/Qualifiers
XX 1..109
FT Region
FT /note= "109 C-terminal residues of human GDF-8"
FT 110..124
FT Region
FT /note= "tetanus toxoid P2 epitope"
FT 125..145
FT Region
FT /note= "tetanus toxoid P30 epitope"
FT 146..254
FT Region
FT /note= "109 C-terminal residues of human GDF-8"
FT 90..91
FT Misc-difference
FT /note= "optionally replaced by Glu-Gly"
FT 235..236
FT Misc-difference
FT /note= "optionally replaced by Glu-Gly"
PN WO200105820-A2.
XX
XX 25-JAN-2001.
PD
XX
XX 20-JUL-2000; 2000WO-DK00413.
PF
XX 20-JUL-1999; 99DK-0001014.
PR 26-JUL-1999; 99US-0145275.
XX
XX (MEBI-) M & E BIOTECH AS.
XX
XX Halkier T, Mouritsen S, Klysner S.
PI WPI: 2001-112680/12.
DR
XX
XX Increasing the muscle mass of animals used in meat production by down
PT regulating growth differentiation factor 8 (GDF-8) activity in the
PT animal through induction of anti-GDF-8 antibody production -
XX
XX Example 1; Page 105-106; 110pp; English.
PS
XX
XX The present sequence is that of AutoVac construct GDF-8 dimer
CC comprising 2 copies of the 109-amino acid C-terminal region of human
CC growth differentiation factor 8 (GDF-8; see AAF20141) covalently
CC connected through the P2 and P30 T-cell epitopes (see AAB20143-44)
CC of tetanus toxin. It is an object of the invention to produce a
CC recombinant therapeutic vaccine that is capable of effecting
CC down-regulation of GDF-8 in order to increase the muscle growth
CC rate of farm animals. The vaccines (see AAB20145-53) are capable
CC of breaking autotolerance against autologous GDF-8. They comprise
CC the C-terminal portion of human GDF-8 in which a portion of the
CC native sequence is replaced by a T-cell epitope such as P30, with
CC minimal disturbance of the authentic 3-dimensional structure of
CC the protein. Nucleic acids encoding the GDF-8 variants can be used
CC for genetic immunisation of the animals. Down-regulation of GDF-8
CC activity can increase muscle mass by up to at least 45% in cattle,
CC pigs and poultry used for meat production, reducing the need for
CC antibiotic feed-additives. Anti-GDF8 vaccines can be used to
CC treat human diseases such as cancer cachexia where muscle atrophy is
CC pronounced and for patients suffering from acute and chronic heart
CC failure.
CC
XX Sequence 254 AA;
SQ
Query Match 85.2%; Score 530.5; DB 22; Length 254;
Best Local Similarity 42.9%; Pred. No. 9,9e-50;
Matches 109; Conservative 0; Mismatches 0; Indels 145; Gaps 2;
QY 1 DFGIDCDDEHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANYGSGCEE----- 48
DB 1 DFGIDCDDEHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANYGSGEEFVLQKYPHTL 60
QY 49 ----- 48
DB 61 VHQANPRGSAGPCCPTPKMSPINMLYFNKGKQIILYKIPAMVYDRGCGSQYIKANSKFTG 120
QY 49 -----FNNFTVSFWLRYPKVSASHLE----- 69
```

```

Db      121 ITELNNFTVSFWLVPKVSASHLEDFGLDCDEHSTESRCRYPPLTVDFEAFGMDWIAP 180
Oy      70 -----AGPCCTPTKMSPTNMLYFNKEQIIT 95
Db      181 KRYKANYSGCEFEVLQKYPHTLVHQANPRGSAGPCCTPTKMSPTNMLYFNKEQIIT 240
Oy      96 KIPAMVVDRCGCS 109
        IITTTTTTTTTT
Db      241 KIPAMVVDRCGCS 254

RESULT 3
AAY33845
ID      AAY33845 standard; Protein: 375 AA.
XX
AC      AAY33845;
XX
DT      08-DEC-1999 (first entry)
XX
DE      Amino acid sequence of Ovine Growth Differentiation Factor-8.
XX
KW      growth differentiation factor; tissue growth; muscle growth;
KW      cell differentiation; animal feed; muscle disorder;
KW      bone degeneration; nerve degeneration; GDF-8; development;
KW      transforming growth factor beta; TGF-beta.
XX
OS      Ovis aries.
XX
PN      M099940181-A1.
XX
PD      12-AUG-1999.
XX
PE      05-FEB-1999; 99WO-US02511.
XX
PR      28-JUL-1998; 98US-0124180.
PR      05-FEB-1998; 98US-0019070.
XX
PA      (UVCJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI      Lee S, McPherron AC;
XX
DR      WPI; 1999-494289/41.
DR      N-PSDB; AA206459.
XX
PT      New differentiation factor useful for treating neurodegenerative
PT      diseases
XX
PS      Example 9; Fig 14g; 138pp; English.
XX
XX      This is the amino acid sequence of the Ovine Growth
CC      Differentiation Factor-8 (GDF-8). Skeletal muscle cDNA libraries from
CC      this species were screened with the murine GDF-8 probe, in order to
CC      isolate the GDF-8. The absolute conservation of the C-terminal region
CC      between species as evolutionary far apart as humans and chickens,
CC      baboons and turkeys, suggests that this region will be highly conserved
CC      in many other species as well.
CC      GDF-8 has been shown to result in increased bone and muscle mass (such
CC      as ribs) when expressed in reduced amounts. GDF-8 minus transgenic
CC      animals and forms of animal feed that can inhibit/reduce production of
CC      GDF-8 are of commercial interest.
CC      GDF-8 expression may also have a role in the therapy of abnormal growth
CC      of muscle, bone or adipose tissue. A GDF-8 monoclonal antibody, GDF-8
CC      antisense molecule or dominant negative polypeptide could be used with
CC      foetal or adult muscle cells, bone cells or progenitor cells. These
CC      agents can be administered to a patient suffering from a disorder such
CC      as muscle wasting disease, neuro muscular disorder, muscle atrophy,
CC      osteoporosis, bone degenerative diseases, obesity or other adipocyte
CC      cell disorders, and aging for example.
XX
SQ      Sequence 375 AA;

```

Query Match 80.9%; Score 504; DB 20; Length 375;

```

        Best Local Similarity 79.5%; Pred. No. 1,2e-46;
Matches 93; Conservative 2; Mismatches 6; Indels 16; Gaps 2;

Oy      1 DFGDCDEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYSGCEFEVLSWLVAY 60
        IITTTTTTTTTT
Db      267 DFGDCDEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYSGCEFE-----LPL 318
Oy      61 PKVSASHL-----EAGPCCTPTKMSPTNMLYFNKEQIITGKIPAMVVDRCGCS 109
        IITTTTTTTTTT
Db      319 QKYPHTLVHQANPKGSAGPCCTPTKMSPTNMLYFNKEQIITGKIPAMVVDRCGCS 375

RESULT 4
AAB20141
ID      AAB20141 standard; Protein: 109 AA.
XX
AC      AAB20141;
XX
DT      30-APR-2001 (first entry)
XX
DE      Human growth differentiation factor 8 C-terminal region.
XX
KW      Growth differentiation factor 8; GDF-8; myostatin; down-regulation;
KW      vaccine; muscle; meat; cachexia; cardiact; human; mutant; mutein.
XX
OS      Homo sapiens.
XX
PN      W0200105820-A2.
XX
PD      25-JAN-2001.
XX
PE      20-JUL-2000; 2000MO-DK00413.
XX
PR      20-JUL-1999; 99DK-0001014.
PR      26-JUL-1999; 99US-0145275.
XX
PA      (MEBI-) M & E BIOTECH AS.
XX
PI      Halkier T, Mouritsen S, Klysner S;
XX
DR      WPI; 2001-112680/12.
XX
PT      Increasing the muscle mass of animals used in meat production by down
PT      regulating growth differentiation factor 8 (GDF-8) activity in the
PT      animal through induction of anti-GDF-8 antibody production -
XX
PS      Claim 17; Page 93-94; 110pp; English.
XX
XX      The present sequence comprises the 109 amino acid residue
CC      C-terminal region of human growth differentiation factor 8
CC      (GDF-8), i.e. residues 267-375 of the full-length protein (see
CC      AAB20131). The homodimer of this region is thought to be the
CC      biologically active form of GDF-8. It is an object of the
CC      invention to produce a recombinant therapeutic vaccine capable of
CC      effecting down-regulation of GDF-8 in order to increase the muscle
CC      growth rate of farm animals. Variants of GDF-8 (see AAB20145-53)
CC      are provided that are capable of breaking autotolerance against
CC      autologous GDF-8. These comprise the C-terminal portion of human
CC      GDF-8 in which a portion of the native sequence is replaced by a
CC      T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
CC      P2 or P30. The high number (9) of Cys residues in the C-terminal
CC      region limits the possible sites in which the T-cell epitope can be
CC      positioned without major disturbance of the native 3-dimensional
CC      structure of the protein. Nucleic acids encoding the GDF-8 variants
CC      can be used for genetic immunisation of the animals. Down-regulation
CC      of GDF-8 activity can increase muscle mass by up to at least 45% in
CC      cattle, pigs and poultry used for meat production, reducing the need
CC      for antibiotic feed-additives. Anti-GDF8 vaccines can be used to
CC      treat human diseases such as cancer cachexia where muscle atrophy is
CC      pronounced and for patients suffering from acute and chronic heart
CC      failure.
XX

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Seq	Sequence	109 AA:
Qy	Query Match	80.4%; Score 501; DB 22; Length 109;
Db	Best Local Similarity	80.7%; Pred. No. 6.2e-47;
Matches	92; Conservative	1; Mismatches 11; Indels 10; Gaps 2
Qy	1 DGLDDEHSTESRCCRYPLTVDFEAFGMDWIIAPRRYKANCSCGCEFFNNFTVSFWLRV 60	
Db	1 DGLDDEHSTESRCCRYPLTVDFEAFGMDWIIAPRRYKANCSCGCEFF----VFLQKY 55	
Qy	61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNKGKQIITGKIPAMVVDRCGCS 109	
Db	56 PHTHLVHQAHPGASAGPCCTPTKMSPINMLYFNKGKQIITGKIPAMVVDRCGCS 109	
RESULT 5		
AAM51935		
ID	AAM51935 standard; protein; 109 AA.	
XX		
AC	AAM51935;	
XX		
DT	01-FEB-2002 (first entry)	
XX		
DE	Human TGFbeta protein superfamily protein GDP8.	
XX		
KM	Human; TGFbeta; transforming growth factor beta; mutant; antagonist;	
KM	agonist; ectopic bone formation; psoriasis; muscular atrophy; scar;	
KM	formation; fibrosis; cirrhosis; osteopathic; antipsoriatic;	
KW	antifibrotic; hepatotropic; vulnery; GDF8.	
XX		
OS	Homo sapiens.	
XX		
PN	DE10026713-A1.	
XX		
PD	06-DEC-2001.	
XX		
PE	30-MAY-2000; 2000DE-1026713.	
XX		
PR	30-MAY-2000; 2000DE-1026713.	
XX		
PA	(SEBA/) SEBALD W.	
XX		
PI	Sebald W, Nickel J;	
XX		
DR	WPI; 2002-042559/06.	
XX		
PT	New mutlein of transforming growth factor-beta superfamily protein,	
PT	useful for treating or preventing e.g. ectopic bone formation, competes	
PT	for receptor binding -	
XX		
PS	Disclosure; Fig 6; 54pp; German.	
XX		
CC	The present invention relates to muteins of a chain of a protein which,	
CC	when in the form of a homodimer, has antagonistic or partial agonistic	
CC	activity, and where the mutation results in the protein binding with low	
CC	affinity to its receptor. The protein is a member of the transforming	
CC	growth factor beta (TGFbeta) superfamily. The mutant sequences of the	
CC	invention can be used in the treatment of diseases associated with the	
CC	overexpression of TGFbeta family proteins, including ectopic bone	
CC	formation, psoriasis, muscular atrophy, scar formation, fibrosis and	
CC	cirrhosis. The present sequence is the human GDP8 protein.	
XX		
SQ	Sequence 109 AA;	
Qy	Query Match	80.4%; Score 501; DB 22; Length 109;
Db	Best Local Similarity	80.7%; Pred. No. 6.2e-47;
Matches	92; Conservative	1; Mismatches 11; Indels 10; Gaps 2;
Qy	1 DFLGDCDHSSTESRCCRYPLTVDFEAFGMDWIIAPRRYKANCSCGCEFFNNFTVSFWLRV 60	
Db	1 DFLGDCDHSSTESRCCRYPLTVDFEAFGMDWIIAPRRYKANCSCGCEFF----VFLQKY 55	
Qy	61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNKGKQIITGKIPAMVVDRCGCS 109	
Db	56 PHTHLVHQAHPGASAGPCCTPTKMSPINMLYFNKGKQIITGKIPAMVVDRCGCS 109	

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Db      56 PHTHVLVHQANPRGSAGPCTPTKMSIFIMNLTFNGKEQIIITGKITPAWYVDRCGCS 109
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
RESULT 6
AAR63161
ID      AAR63161 standard; Protein; 126 AA.
XX
AC      AAR63161;
XX
DT      23-JUN-1995 (first entry)
XX
DE      Mouse growth differentiation factor-8 partial sequence.
XX
KW      Growth differentiation factor-8; GDF-8; cell proliferation;
KM      adipocyte; obesity; transforming growth factor-beta.
XX
OS      Mus musculus.
XX
PN      WO9421681-A.
XX
PD      29-SEP-1994.
XX
PF      18-MAR-1994; 94WO-US03019.
XX
PR      19-MAR-1993; 93US-0033923.
XX
PA      (UUYO ) UNIV JOHNS HOPKINS SCHOOL MED.
XX
PI      Lee S, McPherron AC;
XX
DR      WPI; 1994-316943/39.
XX
DQ      Q-PSTB; Q76380.
XX
PT      New growth differentiation factor 8 - useful for treatment and
PS      diagnosis of cell proliferative disorders esp. of muscle.
XX
PS      Disclosure; Page 41; 84pp; English.
XX
CC      GDF-8 can be used to maintain cells before transplantation; to
CC      improve efficiency of cell fusion and to treat obesity or diseases
CC      related to abnormal adipocyte proliferation.
XX
SO      Sequence 126 AA;

Query Match          80.4%; Score 501; DB 15; Length 126;
Best Local Similarity 80.7%; Pred. No. 7,3e-47;
Matches   92; Conservative    1; Mismatches  11; Indels   10; Gaps     2;

Cy      1 DFGLDCCDEHSTSRCCRPPLYVFDEFAGWDIAPKRKYATCSEGEFNNFTVSFFMLRY 60
Db      18 DFGLDCCDEHSTSRCCRPPLYVFDEFAGWDIAPKRKYATCSEGECEP----VFLQKY 72
        :                               :
Cy      61 PKVASASHL-----EAGPCCTPTKMSPIINMLYENGKEQIIITGKITPAWYVDRCGCS 109
        |       |               |||||
Db      73 PHTHVLVHQANPRGSAGPCTPTKMSPIINMLTFNGKEQIIITGKITPAWYVDRCGCS 126

RESULT 7
AAW69883
ID      AAW69883 standard; Protein; 126 AA.
XX
AC      AAW69883;
XX
DT      07-DEC-1998 (first entry)
XX
DE      Murine growth differentiation factor-8 C-terminal fragment.
XX
KW      Growth differentiation factor-8; GDF-8; mouse; transgenic animal;
KM      transforming growth factor-beta; muscle; meat; inhibitor; obesity;
KM      neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;
therapy.
XX
```


OS Mus -ip. Location/Qualifiers
 FH Key 13..14
 FT Cleavage-site 16..17
 FT Cleavage-site 17..126
 FT Protein /note="mature polypeptide"
 PN W09833887-A1.
 XX
 XX
 PD 06-AUG-1998.
 XX
 PF 05-FEB-1998: 98MO-US02479.
 XX
 PR 23-MAY-1997: 97US-0862445.
 PR 05-FEB-1997: 97US-0795071.
 PR 28-APR-1997: 97US-0847910.
 XX
 XX (UIC0) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 PI Lee S, McPherron AC;
 XX WPI: 1998-437444/37.
 DR N-PSDB: AAV45809.
 XX
 XX Transgenic animals with gene for growth differentiation factor-8
 PT disrupted - have increased muscle and reduced cholesterol contents,
 PT also use of GDF-8 inhibitors for treating cancer, obesity,
 PT neuromuscular disease
 XX
 PS Example 2: Page 58: 125pp: English.
 XX
 CC This is the amino acid sequence of the C-terminal portion of mouse
 CC growth differentiation factor-8 (GDF-8), a novel member of the
 CC transforming growth factor-beta superfamily that appears to relate
 CC to various cell proliferative disorders, especially those involving
 CC muscle, nerve and adipose tissue. The sequence was deduced from a
 CC partial genomic clone (see AAV45809). A full-length sequence (see
 CC AAW30689) has been deduced from a cDNA clone (see AAV42113). The
 CC invention provides novel mammalian and avian GDF-8 proteins (see
 CC AAW69883-92). A transgenic non-human animal is claimed in which
 CC GDF-8 expression is disrupted or interfered with. Also claimed
 CC are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb
 CC from these animals; (2) method for increasing muscle mass in
 CC animals by administering an antibody (Ab) that binds to GDF-8; (3)
 CC inhibiting the action of GDF-8 by treating foetal or adult muscle
 CC or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic
 CC acid encoding a GDF-8 protein truncated by loss of the C-terminal
 CC active fragment. The transgenic animals have increased muscle mass
 CC and for poultry reduced cholesterol contents. Method (3) is used
 CC to treat muscle wasting or neuromuscular diseases, muscular atrophy
 CC and aging, particularly muscular dystrophy, spinal cord or
 CC traumatic injuries, congestive or obstructive lung disease, AIDS
 CC and cachexia. Method (4) is used to treat cancer of muscle,
 CC connective tissue and bone, or obesity. Also (not claimed) GDF-8
 CC can be used to maintain myoblasts intended for transplanting or to
 CC improve efficiency of fusion. Ab can be used to detect and
 CC quantify GDF-8 (particularly in muscle, for diagnosis or monitoring),
 CC also for immunotherapy and in vivo imaging.
 XX
 SQ Sequence 126 AA:
 Query Match 80.4%; Score 501; DB 19: Length 126;
 Best Local Similarity 80.7%; Pred. No. 7, 3e-47;
 Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;
 OY 1 DFGIDCDHSTESRCRCRPLTVDFEAFGMDWIIAPKRYKANYCGSECFNNFTVSWLRY 60
 DB 18 DFGIDCDHSTESRCRCRPLTVDFEAFGMDWIIAPKRYKANYCGSECFNNFTVSWLRY 72
 OY 61 PVSASH- ----EAGPCCTPTKSPINMLYFNKGEQIIYKIKPAMVYDRCGCS 109
 DB 73 PTHLHVHOANPRGSGAGPCCTPTKSPINMLYFNKGEQIIYKIKPAMVYDRCGCS 126

RESULT 8
 AAV15386
 ID AAV15386 standard; Protein: 126 AA.
 XX
 XX AAV15386;
 AC
 XX
 XX 08-DEC-1999 (first entry)
 DE
 XX
 XX C-terminal region of mouse Growth Differentiation Factor-8 (GDF-8).
 KW growth differentiation factor; tissue growth; muscle growth;
 KW cell differentiation; animal feed; muscle disorder;
 KW bone degeneration; nerve degeneration; GDF-8; development;
 KW transforming growth factor beta; TGF-beta.
 XX
 XX Mus musculus.
 OS
 FH Key Location/Qualifiers
 FT Cleavage-site 13..14
 FT Cleavage-site /label= Potential-proteolytic-cleavage-site
 FT Cleavage-site 16..17
 FT Cleavage-site /label= Potential-proteolytic-cleavage-site
 FT /note="cleavage generates mature protein"
 XX
 XX W09940181-A1.
 XX
 XX 12-AUG-1999.
 XX
 PP 05-FEB-1999: 99MO-US02511.
 XX
 PR 28-JUL-1998: 98US-0124180.
 PR 05-FEB-1998: 98US-0019070.
 DR N-PSDB: AAZ06446.
 XX
 XX Lee S, McPherron AC;
 PI WPI: 1999-494289/41.
 DR N-PSDB: AAZ06446.
 XX
 XX New differentiation factor useful for treating neurodegenerative
 PT diseases
 PT
 PS Example 2: Fig 2a: 138pp: English.
 XX
 CC This is the amino acid sequence of the C-terminal region of the GDF-8
 CC precursor protein. The predicted GDF-8 sequence contains two potential
 CC proteolytic processing sites
 CC Cleavage of the precursor at the second of these sites would generate
 CC a mature C-terminal fragment 109 amino acids in length with a predicted
 CC molecular weight of 12,400.
 CC GDF-8 has been shown to result in increased bone and muscle mass (such
 CC as ribs) when expressed in reduced amounts. GDF-8 minus transgenic
 CC animals and forms of animal feed that can inhibit/reduce production of
 CC GDF-8 are of commercial interest.
 CC GDF-8 expression may also have a role in the therapy of abnormal growth
 CC of muscle, bone or adipose tissue. A GDF-8 monoclonal antibody, GDF-8
 CC antisense molecule or dominant negative polypeptide could be used with
 CC foetal or adult muscle cells, bone cells or progenitor cells. These
 CC agents can be administered to a patient suffering from a disorder such
 CC as muscle wasting disease, neuro muscular disorder, muscle atrophy,
 CC osteoporosis, bone degenerative diseases, obesity or other adipocyte
 CC cell disorders, and aging for example.
 XX
 SQ Sequence 126 AA:
 Query Match 80.4%; Score 501; DB 20: Length 126;
 Best Local Similarity 80.7%; Pred. No. 7, 3e-47;
 Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;
 OY 1 DFGIDCDHSTESRCRCRPLTVDFEAFGMDWIIAPKRYKANYCGSECFNNFTVSWLRY 60

Db 18 DPELDDDEHSTESRCRPLTVDFEAGWDMIIAPRKRYKANYSGECEP-----VFLQRY 72
 QY 61 PKYASHL-----EAGPCCTPTKMSPIINMLYFNKGKQIILYKIRPAMVVDRCGCS 109
 Db 73 PHTHLVHQANPRGSAGPCTPTKMSPIINMLYFNKGKQIILYKIRPAMVVDRCGCS 126

RESULT 9
 AAB73182
 ID AAB73182 standard; Protein: 126 AA.
 XX
 AC AAB73182;
 XX
 DE 11-MAY-2001 (first entry)
 XX
 DE Murine GDF-8 #1.
 XX
 KM Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
 KM neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
 KM muscular dystrophy; musclogenenerative disease; tissue repair;
 KM muscle wasting disease; neuromuscular disorder; spinal cord injury;
 KM traumatic injury; congestive obstructive pulmonary disease.
 XX
 OS Mus sp.
 XX
 PN W0200112777-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US22884.
 XX
 PR 19-AUG-1999; 99US-0378238.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 PI Lee S, McPherron AC;
 XX
 DR WPI: 2001-211209/21.
 DR N-PSDB; AAF63547.
 XX
 PT New substantially purified growth differentiation factor-8 polypeptide,
 PT useful for treating muscle wasting disease, obesity, muscular
 PT dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
 PT and cachexia
 XX
 PS Example 2; Fig 2; 124pp; English.
 XX
 CC The present invention relates to growth differentiation factor-8 (GDF-8)
 CC coding sequences and proteins. The present sequence is a GDF-8 protein,
 CC which was isolated in the present invention. GDF-8 is useful for treating
 CC neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and
 CC muscular dystrophy), musclogenenerative diseases or in tissue repair due
 CC to trauma, obesity and disorders related to abnormal proliferation of
 CC adipocytes. GDF-8 is also useful for treating malignancies of the various
 CC organ systems, particularly cells in muscle or adipose tissues and in
 CC gene therapy for the treatment of cell proliferative or immunological
 CC diseases mediated by GDF-8. In addition, GDF-8 is also useful for
 CC treating muscle wasting disease, neuromuscular disorder, spinal cord
 CC injury, traumatic injury, congestive obstructive pulmonary disease
 CC (COPD), AIDS or cachexia.
 CC
 XX
 SQ Sequence 126 AA:
 Query Match 80.4%; Score 501; DB 22; Length 126;
 Best Local Similarity 80.7%; Pred. No. 7.3e-47;
 Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;
 QY 1 DFGIADDENSTESRCRPLTVDFEAGWDMIIAPRKRYKANYSGECEPNNFTVSMFLRY 60
 Db 18 DPELDDDEHSTESRCRPLTVDFEAGWDMIIAPRKRYKANYSGECEP-----VFLQRY 72
 QY 61 PKYASHL-----EAGPCCTPTKMSPIINMLYFNKGKQIILYKIRPAMVVDRCGCS 109
 Db 61 PKYASHL-----EAGPCCTPTKMSPIINMLYFNKGKQIILYKIRPAMVVDRCGCS 109

Db 73 PHTHLVHQANPRGSAGPCTPTKMSPIINMLYFNKGKQIILYKIRPAMVVDRCGCS 126

RESULT 10
 AAB73189
 ID AAB73189 standard; Protein: 130 AA.
 XX
 AC AAB73189;
 XX
 DE 11-MAY-2001 (first entry)
 XX
 DE Rat GDF-8.
 XX
 KM Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
 KM neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
 KM muscular dystrophy; musclogenenerative disease; tissue repair;
 KM muscle wasting disease; neuromuscular disorder; spinal cord injury;
 KM traumatic injury; congestive obstructive pulmonary disease.
 XX
 OS Rattus sp.
 XX
 PN W0200112777-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US22884.
 XX
 PR 19-AUG-1999; 99US-0378238.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 PI Lee S, McPherron AC;
 XX
 DR WPI: 2001-211209/21.
 DR N-PSDB; AAF63555.
 XX
 PT New substantially purified growth differentiation factor-8 polypeptide,
 PT useful for treating muscle wasting disease, obesity, muscular
 PT dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
 PT and cachexia
 XX
 PS Example 9; Fig 2; 124pp; English.
 XX
 CC The present invention relates to growth differentiation factor-8 (GDF-8)
 CC coding sequences and proteins. The present sequence is a GDF-8 protein,
 CC which was isolated in the present invention. GDF-8 is useful for treating
 CC neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and
 CC muscular dystrophy), musclogenenerative diseases or in tissue repair due
 CC to trauma, obesity and disorders related to abnormal proliferation of
 CC adipocytes. GDF-8 is also useful for treating malignancies of the various
 CC organ systems, particularly cells in muscle or adipose tissues and in
 CC gene therapy for the treatment of cell proliferative or immunological
 CC diseases mediated by GDF-8. In addition, GDF-8 is also useful for
 CC treating muscle wasting disease, neuromuscular disorder, spinal cord
 CC injury, traumatic injury, congestive obstructive pulmonary disease
 CC (COPD), AIDS or cachexia.
 CC
 XX
 SQ Sequence 130 AA:
 Query Match 80.4%; Score 501; DB 22; Length 130;
 Best Local Similarity 80.7%; Pred. No. 7.3e-47;
 Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;
 QY 1 DFGIADDENSTESRCRPLTVDFEAGWDMIIAPRKRYKANYSGECEPNNFTVSMFLRY 60
 Db 22 DFGIADDENSTESRCRPLTVDFEAGWDMIIAPRKRYKANYSGECEP-----VFLQRY 76
 QY 61 PKYASHL-----EAGPCCTPTKMSPIINMLYFNKGKQIILYKIRPAMVVDRCGCS 109
 Db 77 PHTHLVHQANPRGSAGPCTPTKMSPIINMLYFNKGKQIILYKIRPAMVVDRCGCS 130

RESULT 11*	
ID	AAB20153 standard; Protein: 160 AA.
AC	AAB20153
XX	
AC	AAB20153;
XX	
DT	30-APR-2001 (first entry)
XX	
DE	Growth differentiation factor 8 AutoVac construct GDF-8 ext.
XX	
KW	Growth differentiation factor 8; GDF-8; myostatin; tetanus toxin;
XX	T-cell epitope; down-regulation; vaccine; muscle; meat; cachexia;
KW	cardiac; human; mutant; mutein.
XX	
OS	Chimeric - Homo sapiens.
OS	Chimeric - Clostridium tetani.
OS	Synthetic.
XX	
Key	Location/Qualifiers
FT	1..15
FT	/note= "identical to residues 215-230 of human
FT	GDF-8"
FT	
Region	16..36
FT	/note= "tetanus toxoid P30 epitope"
FT	37..51
FT	/note= "tetanus toxoid P2 epitope"
FT	52..160
FT	/note= "identical to residues 267-375 of human
FT	GDF-8"
FT	
Misc-difference 124	/note= "Cys-124 may be substituted by Ser to avoid
FT	disulfide bond formation"
FT	
Misc-difference 141..142	/note= "optionally replaced by Glu-Gly"
FT	
FT	
XX	WO200105820-A2.
XX	
PD	25-JAN-2001.
XX	
PF	20-JUL-2000; 2000MO-DK00413.
XX	
PR	20-JUL-1999; 99DK-0001014.
PR	26-JUL-1999; 99DS-0145275.
XX	
PA	(MEBI-) M & E BIOTECH AS.
XX	
DR	Halkier T, Mouritsen S, Klysnier S;
XX	
XX	WPI: 2001-112680/12.
XX	
PT	Increasing the muscle mass of animals used in meat production by down
PT	regulating growth differentiation factor 8 (GDF-8) activity in the
PT	animal through induction of anti-GDF-8 antibody production
XX	
XX	
PS	Example 1; Page 107-108; 110pp; English.
XX	
CC	The present sequence is that of AutoVac construct GDF-8 ext,
CC	which consists of the C-terminal 160 amino acids of human growth
CC	differentiation factor 8 (GDF-8, see AAF20131) with residues 16-36
CC	substituted by the promiscuous tetanus toxin T-cell epitope P30 (see
CC	AAB20144) and residues 37-51 substituted by tetanus toxin T-cell
CC	epitope P2 (see AAB20143). It is an object of the invention to
CC	produce a recombinant therapeutic vaccine that is capable of effecting
CC	down-regulation of GDF-8 in order to increase the muscle growth
CC	rate of farm animals. The vaccines (see AAB20145-53) are capable
CC	of breaking auto-tolerance against autologous GDF-8. They comprise
CC	the C-terminal portion of human GDF-8 in which a portion of the
CC	native sequence is replaced by a T-cell epitope such as P30, with
CC	minimal disturbance of the authentic 3-dimensional structure of
CC	the protein. Nucleic acids encoding the GDF-8 variants can be used
CC	for genetic immunisation of the animals. Down-regulation of GDF-8
CC	activity can increase muscle mass by up to at least 45% in cattle,
CC	pigs and poultry used for meat production, reducing the need for
CC	

[illegible]

XX Sequence 226 AA; 80.4%; Score 501; DB 22; Length 226;
SQ Best Local Similarity 80.7%; Pred. No. 1.4e-46;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;
QY 1 DFGDGDDEHSTESRCRRPLTVDFEAFGWDWIIAPKRRKANYCGSGCECFNNFTVSFWLRY 60
DB 118 DFGDGDDEHSTESRCRRPLTVDFEAFGWDWIIAPKRRKANYCGSGCECFNNFTVSFWLRY 172
QY 61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNKGEOIITYGKIPAMVYDRGCS 109
DB 173 PHTHLVHOANRGSAGPCCPTPTKMSPINMLYFNKGEOIITYGKIPAMVYDRGCS 226
RESULT 13
AAB20132
ID AAB20132 standard; Protein: 362 AA.
AC AAB20132;
XX 30-APR-2001 (first entry)
DT Turkey growth differentiation factor 8.
XX Turkey growth differentiation factor 8.
DE Growth differentiation factor 8; GDF-8; myostatin; down-regulation;
KM vaccine; muscle; meat; cachexia; cardiomy; turkey.
XX Meleagris gallopavo.
OS WO200105820-A2.
XX 25-JAN-2001.
PD 20-JUL-2000; 2000WO-DK00413.
XX 20-JUL-1999; 99DK-0001014.
PR 26-JUL-1999; 99US-0145275.
XX (MEBI-) M & E BIOTECH AS.
XX Halkier T, Mouritsen S, Klysenner S;
PI WPI: 2001-112680/12.
DR Increasing the muscle mass of animals used in meat production by down
XX regulating growth differentiation factor 8 (GDF-8) activity in the
PT animal through induction of anti-GDF-8 antibody production -
XX Example 1; Page 76-78; 110pp; English.
XX The present sequence is that of turkey growth differentiation factor
CC 8 (GDF-8), also called myostatin. It is an object of the invention
CC to produce a recombinant therapeutic vaccine capable of effecting
CC down-regulation of GDF-8 in order to increase the muscle growth
CC rate of farm animals. Variants of GDF-8 (see AAB20145-53) are
CC provided that are capable of breaking autolysis against
CC autologous GDF-8. These comprise a C-terminal portion of human
CC GDF-8 in which a portion of the native sequence is replaced by a
CC T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
CC P2 or P30. Nucleic acids encoding the GDF-8 variants can be used
CC for genetic immunisation of the animals. Down-regulation of GDF-8
CC activity is used to increase muscle mass by up to at least 45%
CC in cattle, pigs and poultry used for meat production, reducing the
CC need for antibiotic feed-additives. Anti-GDF-8 vaccines can be used
CC to treat human diseases such as cancer cachexia where muscle atrophy
CC is pronounced and for patients suffering from acute and chronic
CC heart failure.
SQ Sequence 362 AA;
Query Match 80.4%; Score 501; DB 22; Length 362;

Best Local Similarity 80.7%; Pred. No. 2.4e-46;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;
QY 1 DFGDGDDEHSTESRCRRPLTVDFEAFGWDWIIAPKRRKANYCGSGCECFNNFTVSFWLRY 60
DB 254 DFGDGDDEHSTESRCRRPLTVDFEAFGWDWIIAPKRRKANYCGSGCECFNNFTVSFWLRY 308
QY 61 PKVSASHL-----EAGPCCTPTKMSPINMLYFNKGEOIITYGKIPAMVYDRGCS 109
DB 309 PHTHLVHOANRGSAGPCCPTPTKMSPINMLYFNKGEOIITYGKIPAMVYDRGCS 362
RESULT 14
AAU75623
ID AAU75623 standard; Protein: 374 AA.
AC AAU75623;
XX 21-MAY-2002 (first entry)
DT Chicken promyostatin.
XX Chicken promyostatin.
DE Chicken; promyostatin; immunomodulator; antidepressant; anorectic;
XX neuroprotective; antidiabetic; growth differentiation factor receptor;
KM myostatin receptor; GDF; muscle tissue; adipose tissue; cachexia;
KM wasting disorder; anorexia; muscular dystrophy; neuromuscular disease;
XX metabolic disorder; obesity; type II diabetes.
XX Gallus gallus.
OS WO200210214-A2.
XX 07-FEB-2002.
PD 26-JUL-2001; 2001WO-US23615.
XX 27-JUL-2000; 2000US-0626896.
PR (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX Lee S, McPherron AC;
PI WPI: 2002-217116/27.
DR N-PSDB; ABR15396.
XX New growth differentiation factor (GDF) receptors and modulators,
PT useful for ameliorating wasting disorders such as cachexia, muscular
PT dystrophy or type II diabetes -
XX Claim 22; Fig 1; 184pp; English.
XX The invention relates to a substantially purified growth differentiation
CC factor (GDF) receptor, specifically a myostatin receptor, or its
CC functional peptide portion. Also described is a method of modulating an
CC effect of myostatin on a cell by contacting the cell with an agent that
CC affects myostatin signal transduction in the cell. The method and the
CC receptor are useful for ameliorating the severity of a pathological
CC condition characterised by an abnormal amount, development or metabolic
CC activity of muscle or adipose tissue in a subject, particularly a metabolic
CC disorder (e.g. cachexia, anorexia, muscular dystrophy or neuromuscular
CC disease) or a metabolic disorder (e.g. obesity or type II diabetes). The
CC present sequence represents the amino acid sequence of chicken
CC promyostatin.
SQ Sequence 374 AA;
Query Match 80.4%; Score 501; DB 23; Length 374;
Best Local Similarity 80.7%; Pred. No. 2.5e-46;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;
QY 1 DFGDGDDEHSTESRCRRPLTVDFEAFGWDWIIAPKRRKANYCGSGCECFNNFTVSFWLRY 60

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 25, 2003, 15:08:53 ; Search time 33 Seconds
(without alignments)
680.580 Million cell updates/sec

Title: US-09-620-586B-19

Perfect score: 623

Sequence: 1 DFGDDEHSTESRCRCRYPL.....KEQIIYKIPAMVVDNCGCS 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query length	ID	Description
1	501	80.4	162 6 09TSY2	09TSY2 sus scrofa
2	501	80.4	375 6 09GM97	09GM97 equus caball
3	501	80.4	375 6 095J86	095J86 macaca fasc
4	501	80.4	375 13 08UWD8	08UWD8 columba liv
5	501	80.4	375 13 08UWD7	08UWD7 coturnix ch
6	500	80.3	375 13 098SP0	098SP0 gallus gall
7	495	79.3	375 13 08UWD9	08UWD9 anser anser
8	493	79.1	375 6 08UWEO	08UWEO anas platyr
9	490	78.7	375 6 08WNS6	08WNS6 bos taurus
10	487	78.2	185 6 095N11	095N11 capra hircu
11	480	77.0	185 6 09M218	09M218 ovis aries
12	465	74.6	389 13 090YX0	090YX0 ictalurus p
13	464	74.5	385 13 090M05	090M05 sparus aur
14	463	74.3	373 13 090D18	090D18 salmo salar
15	463	74.3	373 13 090ZD2	090ZD2 oncorhynch
16	463	74.3	373 13 090ZD1	090ZD1 oncorhynch

17	463	74.3	376 13 098TR4	098TR4 oreochromis
18	463	74.3	376 13 090WC9	090WC9 morone saxa
19	463	74.3	376 13 090WC8	090WC8 morone amer
20	463	74.3	376 13 090W06	090W06 umbrina cir
21	462	74.2	373 13 090W17	090W17 salmo salar
22	458	73.5	377 13 098TR3	098TR3 morone chry
23	456	73.2	373 13 098UR3	098UR3 salvelinus
24	447	71.7	359 13 080G53	080G53 sparus aur
25	426	68.4	96 13 09W759	09W759 caltrina mos
26	415	66.6	107 6 09BG54	09BG54 sus scrofa
27	293	47.0	78 6 09XS86	09XS86 equus caball
28	286	45.9	58 6 095MF3	095MF3 sus scrofa
29	262	42.1	191 13 098TR4	098TR4 perca flave
30	257	41.3	104 13 090Z79	090Z79 ictalurus p
31	255	40.9	263 13 06QH11	06QH11 umbrina cir
32	253.5	40.7	598 5 09XZ62	09XZ62 dirosophila
33	253.5	40.7	598 5 09Y4F4	09Y4F4 dirosophila
34	230	36.9	370 13 091350	091350 xenopus lae
35	225.5	36.2	349 5 097138	097138 brugia mala
36	221	35.5	395 13 09PM66	09PM66 anguilla ja
37	217.5	34.9	392 13 09PMR8	09PMR8 carassius a
38	217.5	34.9	393 13 090Z61	090Z61 brachydanio
39	215.5	34.6	115 13 09DGF1	09DGF1 cyprinus ca
40	215.5	34.6	115 13 09DGF6	09DGF6 oryzias lat
41	215.5	34.6	426 4 09HBP0	09HBP0 homo sapien
42	214.5	34.4	115 13 09DGE9	09DGE9 cyprinus ca
43	214.5	34.4	119 6 095KPI	095KPI allurus ful
44	214.5	34.4	367 13 091696	091696 xenopus lae
45	214.5	34.4	424 13 098SP9	098SP9 meleagris g

ALIGNMENTS

RESULT 1	ID	Q9TSY2	PRELIMINARY:	PRT:	162 AA.
AC	Q9TSY2				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	Myostatin (Fragment).				
GN	MSTN.				
OS	Sus scrofa (Pig).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
OX	NCBI_TaxID=9823;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20078370; PubMed=10612246;				
RA	Stratell A., Kopecky M.;				
RT	"Genomic organization, sequence and polymorphism of the porcine				
RT	myostatin (GDF8; MSTN) gene."				
RL	Anim. Genet. 30:468-470(1999).				
CC	-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.				
DR	EMBL: AJ237920; CAB40844.1; -.				
DR	HSSP: P18075; 1BMP.				
DR	InterPro: IPR002400; GF_cyskn0t.				
DR	InterPro: IPR001839; TGFb.				
DR	InterPro: IPR001111; TGFb.N.				
DR	Pfam: PF000019; TGF-beta: 1.				
DR	Pfam: PF00688; TGFb-propeptide; 1.				
DR	PRINTS: PR00436; GFCYSKN0T.				
DR	ProDom: PD000357; TGFb; 1.				
DR	SMART: SM00204; TGFb; 1.				
DR	PROSITE: PS00250; TGF_BETA_1; 1.				
KW	Glycoprotein.				
FT	NON_TER				
SQ	SEQUENCE	162 AA;	18290 MW;	FE3535334512856E CRC64;	
Query Match		80.4%;	Score 501;	DB 6;	Length 162;
Best Local Similarity		80.7%;	Pred. No. 8e-53;		
Matches	92;	Conservative	1;	Mismatches	11;
				Indels	10;
				Gaps	2;

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OY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFNNFTVSFWLRV 60
    |||||||
DB 54 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECF-----VFLQKY 108
OY 61 PKVASASHL-----EAGPCCTPTKMSPINMLYFNKGEOIYIGKIPAMVYDRCGCS 109
    |||||||
DB 109 PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNKGEOIYIGKIPAMVYDRCGCS 162

RESULT 2
OY 09GM97 PRELIMINARY; PRT; 375 AA.
AC 09GM97;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Myostatin.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=THROUGHBRED;
RA Hosoyama T., Yamamouchi K., Tojo H., Tachi C.;
RT "Molecular cloning of equine myostatin cDNA and serum level of
RT myostatin in horse.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AB033541; BAB16046.1; -.
DR HSSP; P18075; IBMP.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Glycoprotein.
SQ
SEQUENCE 375 AA; 42736 MW; 6F424ECBE4D9936 CRC64;

Query Match 80.4%; Score 501; DB 6; Length 375;
Best Local Similarity 80.7%; Pred. No. 2e-52;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFNNFTVSFWLRV 60
    |||||||
DB 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECF-----VFLQKY 321
OY 61 PKVASASHL-----EAGPCCTPTKMSPINMLYFNKGEOIYIGKIPAMVYDRCGCS 109
    |||||||
DB 322 PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNKGEOIYIGKIPAMVYDRCGCS 375

RESULT 3
OY 095J86 PRELIMINARY; PRT; 375 AA.
AC 095J86;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Myostatin.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=GASTROCNEMUS;
RA Smock S.L., Owen T.A.;
RT "Cloning of the open reading frame DNA for macaque fascicularis
RT (cynomolgus macaque) myostatin (cDf8).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AY055750; AAL17640.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
KW Glycoprotein.
SQ
SEQUENCE 375 AA; 42722 MW; 2149B46AC7D446E7 CRC64;

Query Match 80.4%; Score 501; DB 6; Length 375;
Best Local Similarity 80.7%; Pred. No. 2e-52;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFNNFTVSFWLRV 60
    |||||||
DB 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECF-----VFLQKY 321
OY 61 PKVASASHL-----EAGPCCTPTKMSPINMLYFNKGEOIYIGKIPAMVYDRCGCS 109
    |||||||
DB 322 PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNKGEOIYIGKIPAMVYDRCGCS 375

RESULT 4
OY 08UWD8 PRELIMINARY; PRT; 375 AA.
AC 08UWD8;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Myostatin.
GN MSTN.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=8932;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck, Goose, Pigeon and Quail.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440863; AAL35277.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
SQ
SEQUENCE 375 AA; 42739 MW; 88296F0AC79476E CRC64;

Query Match 80.4%; Score 501; DB 13; Length 375;
Best Local Similarity 80.7%; Pred. No. 2e-52;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFNNFTVSFWLRV 60
    |||||||
DB 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECF-----VFLQKY 321
OY 61 PKVASASHL-----EAGPCCTPTKMSPINMLYFNKGEOIYIGKIPAMVYDRCGCS 109
    |||||||
DB 322 PHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNKGEOIYIGKIPAMVYDRCGCS 375

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RESULT 5
Q80WD7 PRELIMINARY: PRT: 375 AA.
AC 080WD7;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DE Myostatin.
GN MSTN.
OS Coturnix chinensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Colinus.
OX NCBI_TaxID=46218;
RN (1)
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck, Goose, Pigeon and Quail."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440864; AAL35278.1; -.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001839; TGF-beta.
DR Pfam: PF00019; TGF-beta; 1.
DR ProDom: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00018; EF-hand; UNKNOWN_1.
DR PROSITE: PS00250; TGF-beta; 1.
SQ SEQUENCE 375 AA; 42721 MW; B893B11A42DE0725 CRC64;

Query Match 80.4%; Score 501; DB 13; Length 375;
Best Local Similarity 80.7%; Pred. No. 2e-52;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 1 DFGLCDHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYSGCCFENFTVSFWLRV 60
DB 267 DFGLCDHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYSGCCFENFTVSFWLRV 60
OY 61 PKVSASHL-----EAGPCPTPKMSPINMLYFNGKEOIIYGIKIPAMVYVRCGCS 109
DB 322 PHTHLVHOANPRGSGAPCPTPKMSPINMLYFNGKEOIIYGIKIPAMVYVRCGCS 375

RESULT 6
Q80SP0 PRELIMINARY: PRT: 375 AA.
AC 080SP0;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE Myostatin.
GN MSTN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN (1)
RP SEQUENCE FROM N.A.
RA Zhang Y., Yang W., Zhu D.;
RT "Genomic structure and expression of the chicken GDF-8 during
RT development."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF346599; AAK18000.1; -.
DR HSP; P18075; 18BP.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGF-beta.

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DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-beta; 1.
DR ProDom: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00018; EF-hand; UNKNOWN_1.
DR PROSITE: PS00250; TGF-beta; 1.
KW Glycoprotein.
SQ SEQUENCE 375 AA; 42717 MW; D980E286426EAD4F CRC64;

Query Match 80.3%; Score 500; DB 13; Length 375;
Best Local Similarity 80.7%; Pred. No. 2.6e-52;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 1 DFGLCDHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYSGCCFENFTVSFWLRV 60
DB 267 DFGLCDHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYSGCCFENFTVSFWLRV 60
OY 61 PKVSASHL-----EAGPCPTPKMSPINMLYFNGKEOIIYGIKIPAMVYVRCGCS 109
DB 322 PHTHLVHOANPRGSGAPCPTPKMSPINMLYFNGKEOIIYGIKIPAMVYVRCGCS 375

RESULT 7
Q80WD9 PRELIMINARY: PRT: 375 AA.
AC 080WD9;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DE Myostatin.
GN MSTN.
OS Anser anser (domestic goose).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
OX NCBI_TaxID=8643;
RN (1)
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck, Goose, Pigeon and Quail."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440862; AAL35276.1; -.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001839; TGF-beta.
DR Pfam: PF00019; TGF-beta; 1.
DR ProDom: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00018; EF-hand; UNKNOWN_1.
DR PROSITE: PS00250; TGF-beta; 1.
SQ SEQUENCE 375 AA; 42667 MW; 57DD849D3AA2978C CRC64;

Query Match 79.5%; Score 495; DB 13; Length 375;
Best Local Similarity 79.8%; Pred. No. 1.1e-51;
Matches 91; Conservative 1; Mismatches 12; Indels 10; Gaps 2;

QY 1 DFGLCDHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYSGCCFENFTVSFWLRV 60
DB 267 DFGLCDHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYSGCCFENFTVSFWLRV 60
OY 61 PKVSASHL-----EAGPCPTPKMSPINMLYFNGKEOIIYGIKIPAMVYVRCGCS 109
DB 322 PHTHLVHOANPRGSGAPCPTPKMSPINMLYFNGKEOIIYGIKIPAMVYVRCGCS 375

RESULT 8
Q80WE0 PRELIMINARY: PRT: 375 AA.
AC 080WE0;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DE Myostatin.
GN MSTN.
OS Coturnix chinensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Colinus.
OX NCBI_TaxID=46218;
RN (1)
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck, Goose, Pigeon and Quail."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440864; AAL35278.1; -.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001839; TGF-beta.
DR Pfam: PF00019; TGF-beta; 1.
DR ProDom: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00018; EF-hand; UNKNOWN_1.
DR PROSITE: PS00250; TGF-beta; 1.
SQ SEQUENCE 375 AA; 42721 MW; B893B11A42DE0725 CRC64;

Query Match 80.4%; Score 501; DB 13; Length 375;
Best Local Similarity 80.7%; Pred. No. 2e-52;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 1 DFGLCDHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYSGCCFENFTVSFWLRV 60
DB 267 DFGLCDHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYSGCCFENFTVSFWLRV 60
OY 61 PKVSASHL-----EAGPCPTPKMSPINMLYFNGKEOIIYGIKIPAMVYVRCGCS 109
DB 322 PHTHLVHOANPRGSGAPCPTPKMSPINMLYFNGKEOIIYGIKIPAMVYVRCGCS 375

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DE Myostatin.
GN MSN.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck, Goose, Pigeon and Quail."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF440861; AAL35275.1;
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
SQ SEQUENCE 375 AA; 42817 MW; 1BA7FE5225C23620 CRC64;

Query Match          79.1%; Score 493; DB 13; Length 375;
Best Local Similarity 79.8%; Pred. No. 1.8e-51;
Matches 91; Conservative 1; Mismatches 12; Indels 10; Gaps 2;

OY 1 DFGLCDDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCGSGCECFNFTVSMILRV 60
    |||||
DB 267 DFGLCDDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCGSGCECFNFTVSMILRV 321
    |||||

OY 61 PKYSASHL-----EAGPCCTPTKMSPIINMLYFNKGKEQIIYGIKIPAVYVDRGCS 109
    |||||
DB 322 PHTHLVHOANPRGSAGPCPTPTKMSPIINMLYFNKGKEQIIYGIKIPAVYVDRGCS 375
    |||||

RESULT 9
OQMS6 PRELIMINARY; PRT: 375 AA.
ID OQMS6;
AC OQMS6;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Myostatin.
GN GDF8.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Shibata M., Muramoto T., Aikawa K.;
RT "Genomic organization and sequence of the myostatin gene in bovine."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB076403; BAB79498.1;
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE: PS00250; TGF_BETA_1; UNKNOWN_1.
SQ SEQUENCE 375 AA; 42524 MW; 0EC27616C202F5E6 CRC64;

Query Match          78.7%; Score 490; DB 6; Length 375;
Best Local Similarity 78.9%; Pred. No. 4.3e-51;
Matches 90; Conservative 2; Mismatches 12; Indels 10; Gaps 2;

OY 1 DFGLCDDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCGSGCECFNFTVSMILRV 60
    |||||

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DB 267 DFGLCDDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCGSGCECFNFTVSMILRV 321
OY 61 PKYSASHL-----EAGPCCTPTKMSPIINMLYFNKGKEQIIYGIKIPAVYVDRGCS 109
    |||||
DB 322 PHTHLVHOANPRGSAGPCPTPTKMSPIINMLYFNKGKEQIIYGIKIPAVYVDRGCS 375
    |||||

RESULT 10
OQ5N11 PRELIMINARY; PRT: 185 AA.
ID OQ5N11;
AC OQ5N11;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Myostatin (Fragment).
GN MSN.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Lian Z., Pan Q., Chen H., Jin H., Li N.;
RT "Cloning of intron 2 of the myostatin gene in goat."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AY032689; AAK49790.1;
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; UNKNOWN_1.
KW Glycoprotein.
FT NON_TER 1
FT NON_TER 185
SQ SEQUENCE 185 AA; 20953 MW; 03675B386E9D64D4 CRC64;

Query Match          78.2%; Score 487; DB 6; Length 185;
Best Local Similarity 78.3%; Pred. No. 4.6e-51;
Matches 90; Conservative 2; Mismatches 7; Indels 16; Gaps 2;

OY 1 DFGLCDDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCGSGCECFNFTVSMILRV 60
    |||||
DB 79 DFGLCDDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCGSGCECFNFTVSMILRV 130
    |||||

OY 61 PKYSASHL-----EAGPCCTPTKMSPIINMLYFNKGKEQIIYGIKIPAVYVDRG 107
    |||||
DB 131 QKYPHTHLVHOANPRGSAGPCPTPTKMSPIINMLYFNKGKEQIIYGIKIPAVYVDRG 185
    |||||

RESULT 11
OQWZ18 PRELIMINARY; PRT: 185 AA.
ID OQWZ18;
AC OQWZ18;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Myostatin (Fragment).
GN MSN.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Lian Z., Jin H., Li N.;
RT "Cloning of intron 2 of the myostatin gene in sheep."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AF266758; AAF78069.1;

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DR HSP, p12643; 3BMP.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb.N.
DR Pfam: PF00019; TGF-beta.1.
DR Pfam: PF00688; TGFb-Propeptide.1.
DR ProDom: PD000357; TGFb.1.
DR SMART: SM00204; TGFb.1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Glycoprotein.
FT NON_TER 1 1
FT SEQUENCE 185 AA; 20923 MW; BA9634203A552850 CRC64;

Query Match
Best Local Similarity 77.0%; Score 480; DB 6; Length 185;
Matches 89; Conservative 2; Mismatches 8; Indels 16; Gaps 2;

QY 1 DGLDCDHSRRCRRPLTVDFEAFGMDWIAPKRYKANYCGSECFNNFTVSFWLRV 60
DB DGLDCDHSRRCRRPLTVDFEAFGMDWIAPKRYKANYCGSECFNNFTVSFWLRV 60
QY 61 PKVASHL-----EAGPCCTPTKMSPIINMLYFNKKEQIITYGKIPAMVYDRGC 107
DB 131 QKYPHTLVHQAHPKGSAGPCCTPTKMSPIINMLYFNKKEQIITYGKIPAMVYDRGC 185

RESULT 12
Q90YVO PRELIMINARY; PRT; 389 AA.
AC Q90YVO:
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Myostatin.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxId=7998;
RN [1]
RP SEQUENCE FROM N.A.
RA Kocbas A.M., Liu Z.J.;
RT "Molecular characterization and expression of the myostatin gene from
RT channel catfish (Ictalurus punctatus).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AF396747; AAK84666.1; -.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb.N.
DR Pfam: PF00019; TGF-beta.1.
DR Pfam: PF00688; TGFb-Propeptide.1.
DR ProDom: PD000357; TGFb.1.
DR PROSITE: PS00250; TGF_BETA_1; UNKNOWN_1.
KW Glycoprotein.
SQ SEQUENCE 389 AA; 43600 MW; 569EB952B7E9E173 CRC64;

Query Match
Best Local Similarity 74.6%; Score 465; DB 13; Length 389;
Matches 84; Conservative 8; Mismatches 7; Indels 16; Gaps 2;

QY 3 GLDGCDHSRRCRRPLTVDFEAFGMDWIAPKRYKANYCGSECFNNFTVSFWLRV 62
DB DGLDCDHSRRCRRPLTVDFEAFGMDWIAPKRYKANYCGSECFNNFTVSFWLRV 62
QY 63 VASHL-----EAGPCCTPTKMSPIINMLYFNKKEQIITYGKIPAMVYDRGC 109
DB 335 YPHHTLVNKRANRGTAAGPCCTPTKMSPIINMLYFNKKEQIITYGKIPAMVYDRGC 389

RESULT 13
Q90M05 PRELIMINARY; PRT; 385 AA.
ID Q90M05:
AC Q90M05:

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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Myostatin.
OS Sparus aurata (gilthead sea bream).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Sparidae; Sparus.
OX NCBI_TaxId=8175;
RN [1]
RP SEQUENCE FROM N.A.
RA Maccatrozzo L., Bargelloni L., Radaelli G., Mascarello F.,
RA Patarnello T.;
RT "Characterization of the myostatin gene in the gilthead seabream.
RT Sparus aurata: sequence, genomic structure, and expression pattern.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AF258448; AAK53545.1; -.
DR EMBL: AF258447; AAK53544.1; -.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb.N.
DR Pfam: PF00019; TGF-beta.1.
DR Pfam: PF00688; TGFb-Propeptide.1.
DR ProDom: PD000357; TGFb.1.
DR PROSITE: PS00250; TGF_BETA_1; UNKNOWN_1.
KW Glycoprotein.
SQ SEQUENCE 385 AA; 43704 MW; 18F902CE325A3916 CRC64;

Query Match
Best Local Similarity 74.5%; Score 464; DB 13; Length 385;
Matches 85; Conservative 6; Mismatches 10; Indels 16; Gaps 2;

QY 1 DGLDCDHSRRCRRPLTVDFEAFGMDWIAPKRYKANYCGSECFNNFTVSFWLRV 60
DB DGLDCDHSRRCRRPLTVDFEAFGMDWIAPKRYKANYCGSECFNNFTVSFWLRV 60
QY 61 PKVASHL-----EAGPCCTPTKMSPIINMLYFNKKEQIITYGKIPAMVYDRGC 109
DB 329 QKYPHTLVNKRANRGSAAGPCCTPTKMSPIINMLYFNKKEQIITYGKIPAMVYDRGC 385

RESULT 14
Q9DD18 PRELIMINARY; PRT; 373 AA.
AC Q9DD18:
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Myostatin precursor.
GN GDF-8.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxId=8030;
RN [1]
RP SEQUENCE FROM N.A.
RA Ostbye T.K., Galloway T.F., Nielsen C., Gabestad I., Bardal T.;
RT "The two myostatin genes of Atlantic salmon (Salmo salar) are
RT expressed in a variety of tissues.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Andersen O.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ostbye T.K., Galloway T.F., Nielsen C., Gabestad I., Bardal T.,
RA Andersen O.;
RT "The two myostatin genes of Atlantic salmon (Salmo salar) are
RT expressed in a variety of tissues.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

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OM protein - protein search, using sw model

Run on: March 25, 2003, 15:03:23 ; Search time 12 seconds
(without alignments)
376.743 Million cell updates/sec

Title: US-09-620-586b-19

Perfect score: 623

Sequence: 1 DGLDGDHSTESRCCRYPL.....KEQIITYKIPANVYDRCCGS 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501	80.4	375	1	GDF8_CHICK
2	501	80.4	375	1	GDF8_HUMAN
3	501	80.4	375	1	GDF8_MELGA
4	501	80.4	375	1	GDF8_PIG
5	501	80.4	376	1	GDF8_MOUSE
6	501	80.4	376	1	GDF8_RAT
7	500	80.3	375	1	GDF8_SHEEP
8	495	79.5	375	1	GDF8_PAPHA
9	490	78.7	375	1	GDF8_BOVIN
10	468	75.1	374	1	GDF8_BRARE
11	467	75.0	405	1	GDF8_MOUSE
12	467	75.0	407	1	GDF8_HUMAN
13	420	67.4	345	1	GDF8_RAT
14	228	36.6	255	1	HBH_MOUSE
15	219	35.2	391	1	HBH_CHICK
16	218	35.0	349	1	HBH_PIG
17	218	35.0	407	1	HBH_BOVIN
18	218	35.0	408	1	HBH_HUMAN
19	216.5	34.8	352	1	HBH_MOUSE
20	215.5	34.6	424	1	HBH_MOUSE
21	215.5	34.6	424	1	HBH_PIG
22	215.5	34.6	424	1	HBH_BOVIN
23	215.5	34.6	425	1	HBH_RAT
24	215.5	34.6	425	1	HBH_MOUSE
25	215.5	34.6	426	1	HBH_HUMAN
26	214	34.3	350	1	DAF7_CABEL
27	213.5	34.3	351	1	HBH_RAT
28	212.5	34.1	207	1	BMP6_RAT
29	212.5	34.1	513	1	BMP6_HUMAN
30	211.5	33.9	352	1	HBH_HUMAN
31	211.5	33.9	426	1	HBH_HORSE
32	210.5	33.8	510	1	BMP6_MOUSE
33	206.5	33.1	424	1	HBH_CHICK

34	205	32.9	355	1	DVR1_BRARE	P35621 brachydanio
35	204.5	32.8	125	1	GDF6_MOUSE	P43028 mus muscu
36	204.5	32.8	436	1	GDF6_BOVIN	P5106 bos taurus
37	203.5	32.7	151	1	GDF7_MOUSE	P43029 mus muscu
38	203	32.6	393	1	BMP2_MOUSE	P49001 ratu
39	203	32.6	394	1	BMP2_RAT	P49001 ratu
40	203	32.6	395	1	BMP2_MOUSE	P49001 ratu
41	203	32.6	396	1	BMP2_DAMDA	P49001 ratu
42	203	32.6	396	1	BMP2_HUMAN	P49001 ratu
43	202	32.4	353	1	BMP2_CHICK	P49001 ratu
44	202	32.4	398	1	BMPA_XENLA	P25703 xenopus
45	202	32.4	398	1	BMPB_XENLA	P30884 xenopus

ALIGNMENTS

Query Match	Best Local Similarity	Score 501; DB 1; Length 375;
80.4%;	80.7%;	Pred. No. 3.1e-48;
AC	042220:	STANDARD; PRT; 375 AA.
DT	15-JUL-1999 (Rel. 38, Last sequence update)	
DT	15-JUL-1999 (Rel. 38, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).	
GN	GDF8 OR MSTN.	
OS	Gallus gallus (Chicken).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	
OC	Gallus.	
OX	NCBI_TaxID=9031;	
RA	SEQUENCE FROM N.A.	
RC	STRAIN=White Leghorn; TISSUE=Skeletal muscle;	
RX	MEDLINE=98024153; PubMed=9356471;	
RA	McPherron A.C., Lee S.-I.,	
RT	"Double muscling in cattle due to mutations in the myostatin gene."	
RL	Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).	
CC	-1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL	
CC	MUSCLE GROWTH.	
CC	-1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).	
CC	-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation-	
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CC	or send an email to license@isb-sdb.ch).	
CC	-----	
DR	EMBL; AF019621; AAB86688.1; --	
DR	HSSP; P18075; 1BMP.	
DR	InterPro: IPR001839; TGFp.	
DR	InterPro: IPR001111; TGFp.N.	
DR	Pfam: PF00019; TGF-beta; 1.	
DR	Pfam: PF00688; TGFp-propeptide; 1.	
DR	ProDom: PD000357; TGFp; 1.	
DR	SMART: SM00204; TGFp; 1.	
DR	PROSITE: PS00250; TGF_BETA.1; 1.	
KW	Growth factor; Cytokine; Glycoprotein; Signal.	
FT	SIGNAL	1
FT	PROPEP	24
FT	CHAIN	267
FT	DISULFID	281
FT	DISULFID	309
FT	DISULFID	313
FT	DISULFID	339
FT	CARBOHD	71
SO	SEQUENCE	375 AA; 42707 MW; DA732DB9426E4DAF CRC64;

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OY      1' DGLDGDHSTESRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGECEFNFTVSFWLRY 60
      |||||||
Db      267 DRLDGDDEHSTESRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECF-----VFLQRY 321

OY      61 PKVSASHL-----EAGPCTPTPKMSPINMLYFNKGEOIITYGKIPAMVYDRCGCS 109
      |||||||
Db      322 PHTHLVHQANPRGASAGPCTPTPKMSPINMLYFNKGEOIITYGKIPAMVYDRCGCS 375

RESULT 4
GDF8_PIG
ID      GDF8_PIG      STANDARD:      PRT:      375 AA.
AC      018831;
DT      15-JUL-1999 (Rel. 38, Created)
DT      15-JUL-1999 (Rel. 38, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN      GDF8 OR MSTN.
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-Skeletal muscle;
RX      MEDLINE=98024153; PubMed=9356471;
RT      McPherron A.C., Lee S.-J.;
RT      "Double muscling in cattle due to mutations in the myostatin gene.";
RT      Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN-Duroc, Hampshire, Meishan, and Yorkshire;
RC      TISSUE-Skeletal muscle;
RA      Voelker G.R., Conroy J.C., Wheeler M.B.;
RT      "Porcine myostatin cDNA sequences: Duroc, Hampshire, Meishan and
RT      Yorkshire pigs.";
RT      Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE OF 1-10 AND 36-375 FROM N.A.
RC      TISSUE-Muscle;
RA      Daneau I., Silversides D.W.;
RT      Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC      -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC      MUSCLE GROWTH.
CC      -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF019623; AAB86690.1; -
DR      EMBL; AF188635; AAF02770.1; -
DR      EMBL; AF188636; AAF02771.1; -
DR      EMBL; AF188637; AAF02772.1; -
DR      EMBL; AF188638; AAF02773.1; -
DR      EMBL; AF033855; AAC08035.1; -
DR      EMBL; AF093798; AAC62489.1; -
DR      HSSP; P18075; IBMP.
DR      InterPro; IPR001839; TGFb.
DR      InterPro; IPR001111; TGFb_N.
DR      Pfam; PF00019; TGF-beta.1.
DR      Pfam; PF00688; TGFb_propeptide; 1.
DR      ProDom; PD000357; TGFb.1.
DR      SMART; SM00204; TGFb.1.
DR      PROSITE; PS00250; TGF_BETA_1.1.
DR      Growth factor; Cytokine; Glycoprotein; Signal.
FT      SIGNAL 1 23 POTENTIAL.

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FT      PROPEP      24      266      POTENTIAL.
FT      CHAIN      267      375      GROWTH/DIFFERENTIATION FACTOR 8.
FT      DISULFID      281      340      BY SIMILARITY.
FT      DISULFID      309      372      BY SIMILARITY.
FT      DISULFID      313      374      BY SIMILARITY.
FT      DISULFID      339      339      INTERCHAIN (BY SIMILARITY).
FT      CARBOHYD      71      71      N-LINKED (GLCNAC...) (POTENTIAL).
SO      SEQUENCE      375 AA; 42791 MW; 0F658685EFD3A348 CRC64;

Query Match      80.4%; Score 501; DB 1; Length 375;
Best Local Similarity 80.7%; Pred. No. 3.1e-48;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY      1 DGLDGDHSTESRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGECEFNFTVSFWLRY 60
      |||||||
Db      267 DRLDGDDEHSTESRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECF-----VFLQRY 321

OY      61 PKVSASHL-----EAGPCTPTPKMSPINMLYFNKGEOIITYGKIPAMVYDRCGCS 109
      |||||||
Db      322 PHTHLVHQANPRGASAGPCTPTPKMSPINMLYFNKGEOIITYGKIPAMVYDRCGCS 375

RESULT 5
GDF8_MOUSE
ID      GDF8_MOUSE      STANDARD:      PRT:      376 AA.
AC      008689;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN      GDF8 OR MSTN.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-CD-1; TISSUE-Skeletal muscle;
RX      MEDLINE=97284412; PubMed=9139826;
RT      McPherron A.C., Lawler A.M., Lee S.-J.;
RT      "Regulation of skeletal muscle mass in mice by a new TGF-beta
RT      superfamily member.";
RT      Nature 387:83-90(1997).
RN      [2]
RP      Nature 387:83-90(1997).
CC      -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC      MUSCLE GROWTH.
CC      -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC      -1- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN DEVELOPING AND ADULT
CC      SKELETAL MUSCLE. WEAK EXPRESSION IN ADIPOSE TISSUE.
CC      -1- DEVELOPMENTAL STAGE: FIRST DETECTED AT DAY 9.5 POST-CONITUM IN
CC      ONE-THIRD OF DEVELOPING SOMITES. AT DAY 10.5, EXPRESSED IN THE
CC      MYOTOME COMPARTMENT OF SOMITES. AT LATER STAGES OF DEVELOPMENT,
CC      DETECTED IN A WIDE RANGE OF DEVELOPING MUSCLES. EXPRESSION
CC      CONTINUES IN ADULthood.
CC      -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U84005; AAC53167.1; -
DR      HSSP; P18075; IBMP.
DR      MGD; MGI:95691; Gdf8.
DR      InterPro; IPR001839; TGFb.
DR      InterPro; IPR001111; TGFb_N.
DR      Pfam; PF00019; TGF-beta.1.
DR      Pfam; PF00688; TGFb_propeptide; 1.
DR      ProDom; PD000357; TGFb.1.
DR      SMART; SM00204; TGFb.1.
DR      PROSITE; PS00250; TGF_BETA_1.1.

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KW Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT PROPEP 25 267 POTENTIAL.
FT CHAIN 268 376 GROWTH/DIFFERENTIATION FACTOR 8.
FT DISULFID 282 341 BY SIMILARITY.
FT DISULFID 310 373 BY SIMILARITY.
FT DISULFID 314 375 BY SIMILARITY.
FT DISULFID 340 340 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 376 AA: 42921 MW: 3819814DD62C08BE CRC64;

Query Match
Best Local Similarity 80.4%; Score 501; DB 1; Length 376;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 1 DGLDGDHSTESRCRRPLTVDFEAFGMDWIIAPKRYKANYSGCECFNNFTVSEWLRV 60
D 268 DGLDGDHSTESRCRRPLTVDFEAFGMDWIIAPKRYKANYSGCECF-----VFLOKY 322
QY 61 PKVASHL-----EAGPCTPTKMSPIINMLYFNKGEOIYIGKIPAMVVDRCGS 109
D 323 PHTHLVHOANPRGSAGPCTPTKMSPIINMLYFNKGEOIYIGKIPAMVVDRCGS 376

RESULT 6
GDF8_RAT
ID GDF8_RAT STANDARD: PRT: 376 AA.
AC 035312.
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL; AF019624; AAB86691.1; -
DR HSSP; P18075; IIMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb.N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb-propeptide; 1.
DR Prodom; PD000357; TGFb.1.
DR SMART; SM00204; TGFb.1.
DR PROSITE; PS00250; TGF-BETA_1; 1.
DR Growth factor; Cytokine; Glycoprotein; Signal.
KM SIGNAL 1 24 POTENTIAL.
FT PROPEP 25 267 POTENTIAL.
FT CHAIN 268 376 GROWTH/DIFFERENTIATION FACTOR 8.
FT DISULFID 282 341 BY SIMILARITY.
FT DISULFID 310 373 BY SIMILARITY.
FT DISULFID 314 375 BY SIMILARITY.
FT DISULFID 340 375 BY SIMILARITY.

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FT DISULFID 340 340 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 376 AA: 42829 MW: 933043DB8C3294B CRC64;

Query Match
Best Local Similarity 80.4%; Score 501; DB 1; Length 376;
Matches 92; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 1 DGLDGDHSTESRCRRPLTVDFEAFGMDWIIAPKRYKANYSGCECFNNFTVSEWLRV 60
D 268 DGLDGDHSTESRCRRPLTVDFEAFGMDWIIAPKRYKANYSGCECF-----VFLOKY 322
QY 61 PKVASHL-----EAGPCTPTKMSPIINMLYFNKGEOIYIGKIPAMVVDRCGS 109
D 323 PHTHLVHOANPRGSAGPCTPTKMSPIINMLYFNKGEOIYIGKIPAMVVDRCGS 376

RESULT 7
GDF8_SHEEP
ID GDF8_SHEEP STANDARD: PRT: 375 AA.
AC 018830.
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Ovis aries (sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL; AF019622; AAB86689.1; -
DR HSSP; P18075; IIMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb.N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb-propeptide; 1.
DR Prodom; PD000357; TGFb.1.
DR SMART; SM00204; TGFb.1.
DR PROSITE; PS00250; TGF-BETA_1; 1.
DR Growth factor; Cytokine; Glycoprotein; Signal.
KM SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 266 POTENTIAL.
FT CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.
FT DISULFID 281 340 BY SIMILARITY.
FT DISULFID 309 372 BY SIMILARITY.
FT DISULFID 313 374 BY SIMILARITY.
FT DISULFID 339 339 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 375 AA: 42827 MW: 1C36F383BB11241 CRC64;

Query Match
80.3%; Score 500; DB 1; Length 375;

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DR InterPro: IPR001111; TGFb_N.
 DR Pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00688; TGFb_propeptide; 1.
 DR ProDom: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 KW Growth factor; Cytokine; Glycoprotein; Signal; Disease mutation.
 FT SIGNAL 1
 FT PROPEP 19
 FT CHAIN 267
 FT DISULFD 281
 FT DISULFD 309
 FT DISULFD 313
 FT DISULFD 339
 FT CARBOHYD 47
 FT CARBOHYD 71
 FT VARIANT 94
 FT VARIANT 113
 FT CONFLICT 14
 SQ SEQUENCE 375 AA; 42551 MM; 84ELAB20650C05F6 CRC64;

Query Match Best Local Similarity 78.7%; Score 490; DB 1; Length 375;
 Matches 90; Conservative 2; Mismatches 12; Indels 10; Gaps 2;

OY 1 DGLDCDDEHSTESRCRPLTVDFEAFGMDWIIAPKRYKANCSCGCEFNFTVSFWLRV 60
 DB 267 DGLDCDDEHSTESRCRPLTVDFEAFGMDWIIAPKRYKANCSCGCEFNFTVSFWLRV 60
 OY 61 PKVASASHL-----EAGPCCTPTKMSPIINMLYFNKGEQIIYGIKIPAMVYDRGCS 109
 DB 322 PHTHLVHGANPRGSAGPCTPTKMSPIINMLYFNKGEQIIYGIKIPAMVYDRGCS 375

RESULT 10
 ID GDF8_BRARE STANDARD; PRT; 374 AA.
 AC 042222;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
 GN GDF8 OR MSTN.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE: Skeletal muscle;
 RX MEDLINE=96024153; PubMed=9356471;
 RA McPherron A.C., Lee S.-J.;
 RT "Double muscling in cattle due to mutations in the myostatin gene";
 RT Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
 CC -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
 CC MUSCLE GROWTH.
 CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC -----
 CC EMBL: AF019626; AA86693.1; -.
 CC HSSP: P18075; IJMP.
 DR ZFIN: ZDB-GENE-990415-165; gdf8.
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR001111; TGFb_N.

DR Pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00688; TGFb_propeptide; 1.
 DR ProDom: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 KW Growth factor; Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1
 FT PROPEP 23
 FT CHAIN 266
 FT DISULFD 280
 FT DISULFD 308
 FT DISULFD 312
 FT DISULFD 338
 FT CARBOHYD 72
 FT CARBOHYD 72
 FT CARBOHYD 274
 SQ SEQUENCE 374 AA; 42060 MM; 6302BC6C8652576 CRC64;

Query Match Best Local Similarity 72.6%; Score 468; DB 1; Length 374;
 Matches 85; Conservative 8; Mismatches 8; Indels 16; Gaps 2;

OY 1 DGLDCDDEHSTESRCRPLTVDFEAFGMDWIIAPKRYKANCSCGCEFNFTVSFWLRV 60
 DB 266 DGLDCDDEHSTESRCRPLTVDFEAFGMDWIIAPKRYKANCSCGCEFNFTVSFWLRV 60
 OY 61 PKVASASHL-----EAGPCCTPTKMSPIINMLYFNKGEQIIYGIKIPAMVYDRGCS 109
 DB 318 QKPYHTLVNKAASRGATGACCTPTKMSPIINMLYFNKGEQIIYGIKIPAMVYDRGCS 374

RESULT 11
 ID GDF8_MOUSE STANDARD; PRT; 405 AA.
 AC 0921M4; 090X55; 09R221;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Growth/differentiation factor 11 precursor (Bone morphogenetic protein 11).
 GN GDF11 OR BMP11.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99177155; PubMed=10075854;
 RA Gamber L.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick R.,
 RA Rosen V.;
 RT "A novel BMP expressed in developing mouse limb, spinal cord, and tail
 RT bud is a potent mesoderm inducer in Xenopus embryos";
 RT Dev. Biol. 208:222-232(1999).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ;
 RX MEDLINE=99318097; PubMed=10391213;
 RA McPherron A.C., Lawler A.M., Lee S.-J.;
 RT "Regulation of anterior/posterior patterning of the axial skeleton by
 RT growth/differentiation factor 11";
 RT Nat. Genet. 22:260-264(1999).
 RL [3]
 RP SEQUENCE OF 75-405 FROM N.A.
 RC MEDLINE=99173787; PubMed=10072786;
 RA Nakashima M., Toyono T., Akamine A., Joyner A.;
 RT "Expression of growth/differentiation factor 11, a new member of the
 RT BMP/Tgfbeta superfamily during mouse embryogenesis";
 RT Mech. Dev. 80:185-189(1999).
 RL [4]
 RP IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
 CC IDENTIFICATION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL
 CC PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
 CC TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.
 CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).

DB 351 QKYPHTLVQANPRGSGAGPCTPTKMSPINMLYFNKQIYKIGFVNVDRGGS 407

RESULT 13

ID GDFB_RAT STANDARD; PRT; 345 AA.

AC Q92217; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Growth/differentiation factor 11 precursor (bone morphogenetic protein 11) (Fragment).
 GN GDF11 OR BMP11.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue-Dental pulp;
 RX MEDLINE=99173787; PubMed=10072786;
 RA Nakashima M., Toyono T., Akamine A., Joyner A.;
 RT "Expression of growth/differentiation factor 11, a new member of the BMP/TGbeta superfamily during mouse embryogenesis.";
 RL Mech. Dev. 80:185-189(1999).
 CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
 CC PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF092733; AAD05266.1; -.
 DR HSSP: P18075; 1BMP.
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR001111; TGFb_N.
 DR Pfam: PF00688; TGFb_propeptide; 1.
 DR ProDom: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 DR Growth factor; Cytokine; Glycoprotein.
 FT NON_TER 1 1
 FT PROPEP <1 242 BY SIMILARITY.
 FT CHAIN 243 >345 GROWTH/DIFFERENTIATION FACTOR 11.
 FT DOMAIN 154 159 POLY-GLY.
 FT DISULFID 257 316 BY SIMILARITY.
 FT DISULFID 315 315 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 38 - 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 345 345
 SQ SEQUENCE 345 AA; 39094 MW; 81D5B93FEDB0443 CRC64;

Query Match 67.4%; Score 420; DB 1; Length 345;

Best Local Similarity 69.4%; Pred. No. 2,7e-39;

Matches 77; Conservative 8; Mismatches 10; Indels 16; Gaps 2;

DB 243 NIGLDCDHSBSRCRPLTVDFASDWIIPKRRKAYVCGGCEY-----MEM 294

QY 61 PVSASHT-----EAGPCTPTKMSPINMLYFNKQIYKIGFVNV 103

DB 295 QKYPHTLVQANPRGSGAGPCTPTKMSPINMLYFNKQIYKIGFVNV 345

RESULT 14

ID IHB_MOUSE STANDARD; PRT; 255 AA.

AC Q04999; 061277; 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Inhibin beta B chain precursor (Activin beta-B chain) (Fragment).
 GN IHB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 1-234 FROM N.A.
 RC STRAIN-CBA X NMRI; Tissue-Testis;
 RX MEDLINE=95344997; PubMed=7619733;
 RA Rivas O., Tuuri T., Eramaa M., Salnio K., Hilden K., Saxen L., Gilbert S.;
 RT "Activin disrupts epithelial branching morphogenesis in developing glandular organs of the mouse.";
 RL Mech. Dev. 50:229-245(1995).
 CC [2]
 CC SEQUENCE OF 134-255 FROM N.A.
 CC MEDLINE=93321614; PubMed=833035;
 CC Albano P.M., Grome N., Smith J.C.;
 RA "Activins are expressed in preimplantation mouse embryos and in ES and EC cells and are regulated on their differentiation.";
 RT Development 117:711-723(1993).
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE, RESPECTIVELY, THE SECRETION OF FOLITROPIN BY THE PITUITARY GLAND.
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION, GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION, ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL, EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF ACTIVINS.
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
 CC ACTIVIN A IS A HOMODIMER OF BETA-A.
 CC ACTIVIN B IS A HOMODIMER OF BETA-B.
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
 CC -1- TISSUE SPECIFICITY: UTERUS, TESTIS, OVARY, LUNG, KIDNEY, BRAIN, CUT EMBRYONIC STEM CELLS, AND POSSIBLY IN LIVER.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC -----
 DR EMBL: X83376; CAA58290.1; -.
 DR EMBL: X69620; CAA49326.1; -.
 DR PIR: S31441; S31441.
 DR HSSP: P12643; 3BMP.
 DR MGD: MGI:96571; Inhb.
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR001111; TGFb_N.
 DR Pfam: PF00019; TGF-beta; 1.
 DR ProDom: PD000357; TGFb; 1.
 DR ProDom: PD000357; TGFb_propeptide; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 DR Growth factor; Hormone; Glycoprotein.
 FT NON_TER 1 1
 FT PROPEP <1 140 POTENTIAL.
 FT CHAIN 141 255 INHIBIN BETA B CHAIN.

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CC -----
DR EMBL; Z71594; CAA96248.1; -.
DR EMBL; AF035478; AAC14187.1; -.
DR EMBL; M61166; AAA48568.1; -.
DR EMBL; M57408; AAA03079.1; -.
DR HSSP; P18075; BMP.
DR InterPro: IPR002400; GF_cysknob.
DR InterPro: IPR001839; TGFB_N.
DR InterPro: IPR001111; TGFB_N.
DR Pfam; PF000019; TGF-beta; 1.
DR Pfam; PF00688; TGF_beta_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD000357; TGFB; 1.
DR SMART; SM00204; TGFB; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Hormone; Glycoprotein; Signal.
FT SIGNAL 1
FT PROPEP 26
FT CHAIN 277
FT DISULFID 280
FT DISULFID 287
FT DISULFID 316
FT DISULFID 320
FT DISULFID 335
FT CARBOHYD 77
FT CONFLICT 30
SQ SEQUENCE 391 AA; 43608 MW; 060017BF33FAF6C CRC64;

Query Match 35.2%; Score 219; DB 1; Length 391;
Best Local Similarity 35.8%; Pred. No. 6.1e-17;
Matches 44; Conservative 18; Mismatches 37; Indels 24; Gaps 4;

QY 3 GLDDDEHSTESRCRYPLTVDFEAFGW-DWIIAPRRKANYCSGCECFENNFVTSFWLRYP 61
   |||| : ||| || |||| | ||| |
Db 277 GLECDGRF--NLCCRQRFYIDRLIGMNDWIITAPSGYGNVCESGSCP-----AYLAGVP 328
   ::||
QY 62 KVSASHLEA-----GPCCTPTKMSPIINMLYENGKRQIITYKRIPAWVDRC 106
   ::||
Db 329 GSASSFHATAVYNQYRMRGILPGTVNSCCIPTKLSTMSMLYFDDEXNIVAKRDVPMNIVEEC 388
   |||
QY 107 GCS 109
   |||
Db 389 GCA 391

Search completed: March 25, 2003, 15:11:38
Job time : 12 secs
```


GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 25, 2003, 15:09:33 ; Search time 43 Seconds
(without alignments)
243.690 Million cell updates/sec

Title: US-09-620-586b-19

Perfect score: 623

Sequence: I DFGIDCDDEHSTESRCRRPL.....KEQIIYKIPAMVYDRGCS 109

Scoring table: BLOSUM62
Gapop.10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	36.9	370	2 I51199	activin beta B sub
2	228	36.6	255	2 I48235	inhibin beta-B cha
3	228	36.6	411	2 B41398	inhibin beta-B cha
4	218	35.0	349	1 WPGGBB	inhibin beta-B cha
5	218	35.0	407	1 A40150	inhibin beta-B cha
6	218	35.0	408	2 S50899	betab inhibin prec
7	217.5	34.9	115	2 PN0506	activin beta B-2 c
8	217.5	34.9	393	2 I50103	activin beta B - z
9	216.5	34.8	115	2 PN0505	activin beta B-1 c
10	216.5	34.8	352	2 JC5366	activin beta C - m
11	216.5	34.6	352	2 S70580	activin beta C pre
12	215.5	34.6	424	1 WPGGBA	inhibin beta-A cha
13	215.5	34.6	424	1 S31440	inhibin beta-A cha
14	215.5	34.6	424	1 B40905	inhibin beta-A cha
15	215.5	34.6	425	1 S50898	inhibin beta-A cha
16	215.5	34.6	425	2 I47072	inhibin beta-A cha
17	215.5	34.6	426	1 B24248	inhibin beta-A cha
18	214.5	34.4	367	2 JC4151	activin beta D cha
19	214	34.3	350	2 T25451	transforming growt
20	212.5	34.1	207	2 S37618	vgr protein - rat
21	212.5	34.1	513	1 BMH06	bone morphogenetic
22	211.5	33.9	352	2 JC2466	inhibin beta-C cha
23	210.5	33.8	510	2 A54798	Vg-1-related prote
24	206	33.1	373	2 PW0042	activin - fruit fl
25	204.5	32.8	125	2 S43295	bone morphogenetic
26	204.5	32.8	426	2 B55452	cartilage-derived
27	203.5	32.7	151	2 S43296	bone morphogenetic
28	203	32.6	393	2 S37073	bone morphogenetic
29	203	32.6	394	2 S45355	bone morphogenetic

30	203	32.6	396	1 BMH02	bone morphogenetic
31	202	32.4	353	2 I50607	bone morphogenetic
32	202	32.4	398	2 JH0688	bone morphogenetic
33	202	32.4	398	2 JH0687	bone morphogenetic
34	201.5	32.3	413	2 JC4862	activin beta-A cha
35	197.5	31.7	452	2 I49542	bone morphogenetic
36	197.5	31.7	454	1 BMH05	bone morphogenetic
37	197.5	31.7	451	2 S52408	SPDVR1 protein - s
38	197	31.6	366	2 A46607	growth/differentia
39	195.5	31.4	313	2 I51284	bone morphogenetic
40	195.5	31.4	360	2 A29619	Vgl embryonic grow
41	195	31.3	360	2 I53032	bone morphogenetic
42	195	31.3	366	2 A45402	transforming growt
43	194.5	31.2	402	2 A45056	osteogenic protein
44	194.5	31.2	426	2 JH0650	bone morphogenetic
45	194.5	31.2	495	2 S43294	bone morphogenetic

ALIGNMENTS

RESULT 1

I51199 activin beta B subunit - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999

C:Accession: I51199

R:Donrman, C.R.; Hemmati-Brivanlou, A.; Thomsen, G.H.; Fields, A.; Woolf, T.M.; Melt

Dev. Biol. 157, 474-483, 1993

A:Title: Expression of activin mRNA during early development in Xenopus laevis.

A:Reference number: I51199; MUID:93273083; PMID:8500654

A:Accession: I51199

A>Status: preliminary: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-370 <DOR>

C:Cross-references: GB:S61773; NID:g386027; PIDN:AA826863.1; PID:g386028

C:Superfamily: inhibin

Query Match

Best Local Similarity 37.4%; Pred. No. >2.7e-17;
Matches 46; Conservative 17; Mismatches 36; Indels 24; Gaps 4;

QY	3	GLDDEHSTESRCRYPTLVDFEAFGW-DWIIAPKRYKANYCSGCEFFNFTVSFWLRVP 61
DB	256	GLECCGHT--NICCRQQRYYIDRLIGMWDIIAPAGYGVNCEGSCP-----AYLAGVP 307
QY	62	KVSASHLEA-----GPCCTPTKMSPTNNLYNGKEQIIYKIPAMVYDRG 106
DB	308	GSASSFHFVAVNQYRMRLINPCTVNSCIPTKLSTMSMLYFDDEYIVKRDVPMIVDEC 367
QY	107	GCS 109
DB	368	GCA 370

RESULT 2

